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Application No.: 09458298

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

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Table VII A
Mage 2_A01 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASEYLQLVF	154	9		1
ASSFSTTINY	68	10	0.1700	2
DLVQENYLEY	249	10		3
ELSMLEVF	224	8		4
ELVHFLLLKY	115	10		5
ESVLRNCQDF	137	10		6
ESVLRNCQDFF	137	11		7
EVFEGREDSVF	229	11		8
EVVPISHLY	168	9	0.0028	9
FSTTINYTLW	71	10		10
GSDPACYEF	263	9		11
GSDPACYEFLW	263	11		12
HSPQGASSF	63	9		13
ILVTCLGLSY	177	10		14
ISRKMVELVHF	109	11		15
KIGGEPHISY	292	10		16
KMVELVHF	112	8		17
LLMQDLVQENY	245	11		18
LMQDLVQENY	246	10	0.0450	19
LVHFLLLKY	116	9		20
LVQENYLEY	250	9		21
LVTCLGLSY	178	9		22
PVIFSKASEY	148	10		23
QVPGSDPACY	260	10		24
RMFPDLESEF	96	10		25
SSFSTTINY	69	9	0.0430	26
STTINYTLW	72	9		27
SVLRNCQDF	138	9		28
SVLRNCQDFF	138	10		29
TTINYTLW	73	8		30
VIFSKASEY	149	9		31
VLRNCQDF	139	8		32
VLRNCQDFF	139	9		33
VTCLGLSY	179	8		34
VVEVVPISHLY	166	11	0.2000	35
VVPISHLY	169	8		36
YILVTCLGLSY	176	11		37

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Table VII B

Mage 3 A01 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASSLPTTMNY	68	10	2.6000	38
ASSSLQLVF	154	9		39
ATCLGLSY	179	8	0.1100	40
ELSVLEVF	224	8		41
ELVHFLLLKY	115	10		42
EMLGSVVGNW	134	10		43
EVDPIGHLY	168	9	18.0000	44
EVDPIGHLYIF	168	11		45
FVQENYLEY	250	9		46
GSDPACYEF	263	9		47
GSDPACYEFLW	263	11		48
GSVVGNWQY	137	9	0.0500	49
GSVVGNWQYF	137	10		50
GSVVGNWQYFF	137	11		51
HISYPPLHEW	298	10		52
ISGGPHISY	293	9	0.0370	53
ISYPPLHEW	299	9		54
KISGGPHISY	292	10	0.0011	55
KVAELVHF	112	8		56
LLTQHFVQENY	245	11		57
LMEVDPIGHLY	166	11	7.5000	58
LSRKVAELVHF	109	11		59
LTQHFVQENY	246	10	0.2600	60
LVHFLLLKY	116	9		61
MLGSVVGNW	135	9		62
MLGSVVGNWQY	135	11		63
PIGHLYIF	171	8		64
PSTFPDLESEF	95	11		65
PTTMNYPLW	72	9		66
QVPGSDPACY	260	10		67
SLPTTMNY	70	8		68
SLPTTMNYPLW	70	11		69
SSLPTTMNY	69	9	0.0550	70
SSSLQLVF	155	8		71
STFPDLESEF	96	10		72
SVVGNWQY	138	8		73
SVVGNWQYF	138	9		74
SVVGNWQYFF	138	10		75
TMNYPLWSQSY	74	11	0.0830	76
TTMNYPLW	73	8		77
VVGNWQYF	139	8		78
VVGNWQYFF	139	9		79
YIFATCLGLSY	176	11		80

Table VIII A
Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
AAISRKMV	107	8						81
AAISRKMVEL	107	10						82
AAISRKMVELV	107	11						83
AIIAIEGDCA	207	10						84
AISRKMVEL	108	9						85
AISRKMVELV	108	10						86
ALGLVGAQA	22	9						87
ALGLVGAQAPA	22	11						88
ALIETSYV	277	8						89
ALIETSYVKV	277	10						90
ALIETSYVKVL	277	11						91
AQAPATEEQQT	28	11						92
ATEEQQTA	32	8						93
CAPEEKIWEEL	215	11						94
CLGLSYDGL	181	9						95
CLGLSYDGLL	181	10						96
CQDFFPVI	143	8						97
DLESEFQA	100	8						98
DLESEFQAA	100	9						99
DLESEFQAAI	100	10						100
DLVQENYL	249	8						101
EALGLVGA	21	8						102
EALGLVGAQA	21	10						103
EARGEALGL	17	9						104
EARGEALGLV	17	10						105
ELVHFLLL	115	8						106
EQQTASSSST	35	10						107
EQQTASSSSTL	35	11						108
ETSYVKVL	280	8						109
ETSYVKVLHHT	280	11						110
EVFEGREDSV	229	10						111
EVTLGEVPA	47	9						112
EVTLGEVPAA	47	10						113
EVVEVVPI	165	8						114
EVVEVVPISHL	165	11						115
EVVPISHL	168	8						116
EVVPISHLYI	168	10						117
EVVPISHLYIL	168	11						118
FAHPRKLL	239	8						119
FAHPRKLLM	239	9						120
FLLLKYRA	119	8						121
FLWGPRAL	271	8						122
FLWGPRALI	271	9						123
FLWGPRALIET	271	11						124
FQAAISRKM	105	9						125
FQAAISRKMV	105	10						126

Table VIII A
Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
GASSFSTT	67	8						127
GASSFSTTI	67	9						128
GIEVVEVV	163	8						129
GIEVVEVVPI	163	10						130
GLEARGEA	15	8						131
GLEARGEAL	15	9						132
GLEARGEALGL	15	11						133
GLLGDNQV	188	8						134
GLLGDNQVM	188	9						135
GLLIIVLA	200	8						136
GLLIIVLAI	200	9						137
GLLIIVLAII	200	10						138
GLLIIVLAIIA	200	11						139
GLSYDGLL	183	8						140
GLVGAQAPA	24	9						141
GLVGAQAPAT	24	10						142
HISYPPLHERA	298	11						143
HLYILVTCL	174	9						144
HLYILVTCLGL	174	11						145
HTLKIGGEPHI	289	11						146
IAIEGDCA	209	8						147
IIAIEGDCA	208	9						148
IIVLAIIA	203	8						149
IIVLAIIAI	203	9						150
ILVTCLGL	177	8						151
IVLAIIAI	204	8						152
KAEMLESV	132	8						153
KAEMLESVL	132	9						154
KASEYLQL	153	8						155
KASEYLQLV	153	9						156
KIGGEPHI	292	8						157
KIWEELSM	220	8						158
KIWEELSML	220	9						159
KIWEELSMLEV	220	11						160
KLLMQDLV	244	8						161
KMVELVHFL	112	9						162
KMVELVHFLL	112	10						163
KMVELVHFLLL	112	11						164
KTGLLIIV	198	8						165
KTGLLIIVL	198	9						166
KTGLLIIVLA	198	10						167
KTGLLIIVLAI	198	11						168
KVLHHTLKI	285	9						169
LAIIAIEGDCA	206	11						170
LIETSYVKV	278	9						171
LIETSYVKVL	278	10						172

Table VIII A
Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
LIIVLAII	202	8						173
LIIVLAIIA	202	9						174
LIIVLAIIAI	202	10						175
LLGDNQVM	189	8						176
LLGDNQVMPKT	189	11						177
LLIIVLAI	201	8						178
LLIIVLAII	201	9						179
LLIIVLAIIA	201	10						180
LLIIVLAIIAI	201	11						181
LLKYRAREPV	121	10						182
LLKYRAREPVT	121	11						183
LLLKYRAREPV	120	11						184
LMQDLVQENYL	246	11						185
LQLVFGIEV	158	9						186
LQLVFGIEVV	158	10						187
LVEVTLGEV	45	9						188
LVEVTLGEVPA	45	11						189
LVFGIEVV	160	8						190
LVFGIEVVEV	160	10						191
LVFGIEVVEVV	160	11						192
LVGAQAPA	25	8						193
LVGAQAPAT	25	9						194
LVHFLLLKYRA	116	11						195
MQDLVQENYL	247	10						196
MVELVHFL	113	8						197
MVELVHFLL	113	9						198
MVELVHFLLL	113	10						199
NQEEEGPRM	89	9						200
NQVMPKTGL	193	9						201
NQVMPKTGLL	193	10						202
NQVMPKTGLLI	193	11						203
PATEEQQT	31	8						204
PATEEQQTA	31	9						205
PISHLYIL	171	8						206
PISHLYILV	171	9						207
PISHLYILVT	171	10						208
PQGASSFST	65	9						209
PQGASSFSTT	65	10						210
PQGASSFSTTI	65	11						211
PVIFSKASEYL	148	11						212
PVTKAEML	129	8						213
PVTKAEMLESV	129	11						214
QAAISRKM	106	8						215
QAAISRKMV	106	9						216
QAAISRKMVEL	106	11						217
QAPATEEQQT	29	10						218

Table VIII A
Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
QAPATEEQQTA	29	11						219
QLVFGIEV	159	8						220
QLVFGIEVV	159	9						221
QLVFGIEVVEV	159	11						222
QQTASSSST	36	9						223
QQTASSSSTL	36	10						224
QQTASSSSTLV	36	11						225
QTASSSST	37	8						226
QTASSSSTL	37	9						227
QTASSSSTLV	37	10						228
QVMPKTGL	194	8						229
QVMPKTGLL	194	9						230
QVMPKTGLLI	194	10						231
QVMPKTGLLII	194	11						232
QVPGSDPA	260	8						233
RALIETSYV	276	9						234
RALIETSYVKV	276	11						235
RAREPVTKA	125	9						236
RAREPVTKAEM	125	11						237
RQVPGSDPA	259	9						238
SQHCKPEEGL	7	10						239
STLVEVTL	43	8						240
STLVEVTLGEV	43	11						241
STTINYTL	72	8						242
SVFAHPRKL	237	9						243
SVFAHPRKLL	237	10						244
SVFAHPRKLLM	237	11						245
TASSSSTL	38	8						246
TASSSSTLV	38	9						247
TASSSSTLVEV	38	11						248
TLGEVPAA	49	8						249
TLKIGGEPHI	290	10						250
TLVEVTLGEV	44	10						251
VIFSKASEYL	149	10						252
VLHHTLKI	286	8						253
VLRNCQDFFPV	139	11						254
VMPKTGLL	195	8						255
VMPKTGLLI	195	9						256
VMPKTGLLII	195	10						257
VMPKTGLLIIV	195	11						258
VQENYLEYRQV	251	11						259
VTCLGLSYDGL	179	11						260
VTKAEMLESV	130	10						261
VTKAEMLESVL	130	11						262
VTLGEVPA	48	8						263
VTLGEVPAA	48	9						264

Table VIII A
Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
VVEVVPISHL	166	10						265
VVPISHLYI	169	9						266
VVPISHLYIL	169	10						267
VVPISHLYILV	169	11						268
YILVTCLGL	176	9						269
YLQLVFGI	157	8						270
YLQLVFGIEV	157	10						271
YLQLVFGIEVV	157	11						272
YVKVLHHT	283	8						273
YVKVLHHTL	283	9						274
YVKVLHHTLKI	283	11						275

Table VIII B

Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
AALSRKVA	107	8						276
AALSRKVAEL	107	10	0.0007					277
AALSRKVAELV	107	11						278
AASSSSTL	38	8						279
AASSSSTLV	38	9	0.0001					280
AASSSSTLVEV	38	11						281
AIIAREGDCA	207	10	0.0002					282
ALGLVGAQA	22	9	0.0030					283
ALGLVGAQAPA	22	11						284
ALSRKVAEL	108	9	0.0050					285
ALSRKVAELV	108	10	0.0001					286
ALVETSYV	277	8						287
ALVETSYVKV	277	10	0.0024					288
ALVETSYVKVL	277	11						289
AQAPATEEQEA	28	11						290
ATCLGLSYDGL	179	11						291
ATEEQEAA	32	8						292
CAPEEKIWEEL	215	11						293
CLGLSYDGL	181	9	0.0004					294
CLGLSYDGLL	181	10	0.0001					295
DLESEFQA	100	8						296
DLESEFQAA	100	9	0.0001					297
DLESEFQAAL	100	10	0.0001					298
EAASSSST	37	8						299
EAASSSSTL	37	9	0.0001					300
EAASSSSTLV	37	10	0.0001					301
EALGLVGA	21	8						302
EALGLVGAQA	21	10	0.0001					303
EARGEALGL	17	9	0.0001					304
EARGEALGLV	17	10	0.0001					305
ELMEVDPI	165	8						306
ELMEVDPIGHL	165	11	0.0260					307
ELVHFLLL	115	8						308
EQEAASSSST	35	10						309
EQEAASSSSTL	35	11						310
ETSYVKVL	280	8						311
ETSYVKVLHHM	280	11						312
EVDPIGHL	168	8						313
EVDPIGHLYI	168	10	0.0002					314
EVFEGREDSI	229	10	0.0001					315
EVFEGREDSIL	229	11						316
EVTLGEVPA	47	9	0.0001					317
EVTLGEVPAA	47	10	0.0001					318
FLLLKYRA	119	8						319
FLWGPRAL	271	8						320
FLWGPRALV	271	9	0.0820	0.0500	0.9100	0.0043	1.1000	321
FLWGPRALVET	271	11						322
FQAALSRKV	105	9						323

Table VIII B

Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
FQAALSRKVA	105	10						324
GASSLPTT	67	8						325
GASSLPTTM	67	9	0.0001					326
GIELMEVDPI	163	10	0.0002					327
GLEARGEA	15	8						328
GLEARGEAL	15	9	0.0001					329
GLEARGEALGL	15	11						330
GLLGDNQI	188	8						331
GLLGDNQIM	188	9						332
GLLIIVLA	200	8						333
GLLIIVLAI	200	9	0.0002					334
GLLIIVLAII	200	10	0.0005					335
GLLIIVLAIIA	200	11						336
GLSYDGLL	183	8						337
GLVGAQAPA	24	9	0.0003					338
GLVGAQAPAT	24	10	0.0004					339
HISYPPLHEWV	298	11						340
HLYIFATCL	174	9	0.0003					341
HLYIFATCLGL	174	11	0.0410	0.0140	0.1500	0.0029	0.1500	342
HMVKISGGPHI	289	11						343
IAREGDCA	209	8						344
IIAREGDCA	208	9	0.0001					345
IIVLAIIA	203	8						346
ILGDPKKL	238	8						347
ILGDPKKLL	238	9	0.0001					348
ILGDPKKLLT	238	10	0.0001					349
IMPKAGLL	195	8						350
IMPKAGLLI	195	9	0.0064					351
IMPKAGLLII	195	10	0.0015					352
IMPKAGLLIIV	195	11	0.0130					353
KAEMLGSV	132	8						354
KAEMLGSVV	132	9	0.0001					355
KAGLLIIV	198	8						356
KAGLLIIVL	198	9	0.0002					357
KAGLLIIVLA	198	10	0.0002					358
KAGLLIIVLAI	198	11						359
KASSSLQL	153	8						360
KASSSLQLV	153	9	0.0005					361
KISGGPHI	292	8						362
KIWEELSV	220	8						363
KIWEELSVL	220	9	0.0140	0.0064	0.0073	0.0590	0.0012	364
KIWEELSVLEV	220	11						365
KLLTQHFV	244	8						366
KVAELVHFL	112	9	0.0550					367
KVAELVHFLL	112	10	0.0120					368
KVAELVHFLLL	112	11						369
KVLHHMVKI	285	9	0.0026					370
LAIIAREGDCA	206	11						371

Table VIII B

Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
LIIVLAII	202	8						372
LIIVLAIIA	202	9	0.0008					373
LLGDNQIM	189	8						374
LLGDNQIMPKA	189	11						375
LLIIVLAI	201	8						376
LLIIVLAII	201	9	0.0001					377
LLIIVLAIIA	201	10	0.0002					378
LLKYRAREPV	121	10	0.0001					379
LLKYRAREPVT	121	11						380
LLLKYRAREPV	120	11	0.0001					381
LMEVDPIGHL	166	10	0.0005					382
LQLVFGIEL	158	9						383
LQLVFGIELM	158	10						384
LTQHFVQENYL	246	11						385
LVETSYVKV	278	9	0.0001					386
LVETSYVKVL	278	10	0.0002					387
LVEVTLGEV	45	9	0.0001					388
LVEVTLGEVPA	45	11						389
LVFGIELM	160	8						390
LVFGIELMEV	160	10	0.1100					391
LVGAQAPA	25	8						392
LVGAQAPAT	25	9	0.0001					393
LVHFLLLKYRA	116	11						394
MVKISGGPHI	290	10	0.0002					395
NQEEEGPST	89	9						396
NQIMPKAGL	193	9						397
NQIMPKAGLL	193	10						398
NQIMPKAGLLI	193	11						399
PATEEQEA	31	8						400
PATEEQEAA	31	9	0.0001					401
PIGHLYIFA	171	9	0.0001					402
PIGHLYIFAT	171	10	0.0003					403
PQGASSLPT	65	9						404
PQGASSLPTT	65	10						405
PQGASSLPTTM	65	11						406
PQSPQGASSL	62	10						407
PTTMNYPL	72	8						408
PVIFSKASSSL	148	11						409
PVTKAEML	129	8						410
PVTKAEMLGSV	129	11						411
QAALSRKV	106	8						412
QAALSRKVA	106	9	0.0001					413
QAALSRKVAEL	106	11						414
QAPATEEQEA	29	10	0.0001					415
QAPATEEQEAA	29	11						416
QIMPKAGL	194	8						417
QIMPKAGLL	194	9	0.0001					418
QIMPKAGLLI	194	10	0.0006					419

Table VIII B
Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
QIMPKAGLLII	194	11						420
QLVFGIEL	159	8						421
QLVFGIELM	159	9	0.0010					422
QLVFGIELMEV	159	11	0.3400					423
QVPGSDPA	260	8						424
RALVETSYV	276	9	0.0001					425
RALVETSYVKV	276	11						426
RAREPVTKA	125	9						427
RAREPVTKAEM	125	11						428
RQVPGSDPA	259	9						429
SILGDPKKL	237	9	0.0001					430
SILGDPKKLL	237	10	0.0002					431
SILGDPKKLLT	237	11						432
SLPTTMNYPL	70	10	0.0035					433
SLQLVFGI	157	8						434
SLQLVFGIEL	157	10	0.0049					435
SLQLVFGIELM	157	11						436
SQHCKPEEGL	7	10						437
STLVEVTL	43	8						438
STLVEVTLGEV	43	11	0.0140					439
TLGEVPAA	49	8						440
TLVEVTLGEV	44	10	0.0250	0.0320	1.6000	0.0039	0.1600	441
TQHFVQENYL	247	10						442
VAELVHFL	113	8						443
VAELVHFLL	113	9	0.0001					444
VAELVHFLLL	113	10	0.0009					445
VIFSKASSSL	149	10	0.0001					446
VLHHMVKI	286	8						447
VQENYLEYRQV	251	11						448
VTKAEMLGSV	130	10	0.0002					449
VTKAEMLGSVV	130	11						450
VTLGEVPA	48	8						451
VTLGEVPAA	48	9	0.0045					452
VVGNWQYFFPV	139	11						453
WQYFFPVI	143	8						454
YIFATCLGL	176	9	0.0180					455
YVKVLHHM	283	8						456
YVKVLHHMV	283	9	0.0001					457
YVKVLHHMVKI	283	11						458

Table IX a
Mage 2 A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
AIEGDCAPEEK	210	11	0.0009	0.0007				459
ALIETSYVK	277	9	0.0810	0.1900	0.0200	0.0003	0.0280	460
DLVQENYLEYR	249	11	0.0047	0.0018				461
DSVFAHPR	236	8	-0.0004	0.0005				462
DSVFAHPRK	236	9	0.0021	0.0025	0.0006	0.0190	0.0460	463
ELSMLEVFEGR	224	11	0.0016	0.0008				464
ELVHFLLLK	115	9	0.0045	0.0011				465
ELVHFLLLKYR	115	11	0.0011	0.0031				466
EMLESVLR	134	8	-0.0009	-0.0003				467
ESEFQAAISR	102	10	0.0002	0.0002				468
ESEFQAAISRK	102	11	0.0010	0.0004				469
FLLLKYRAR	119	9						470
FSTTINYTLWR	71	11	0.0110	0.0170	0.0700	0.0074	0.0490	471
GLLGDNQVMPK	188	11	0.0780	0.0047	-0.0006	-0.0013	-0.0001	472
GSSNQEEEGPR	86	11	-0.0002	-0.0002				473
HISYPPLHER	298	10	0.0074	0.0018				474
ISYPPLHER	299	9	0.0340	0.0280	0.7700	0.8100	0.0990	475
KAEMLESVLR	132	10	0.0002	0.0009	0.0084	0.0047	0.0004	476
KVLHHTLK	285	8	0.0053	0.0100				477
LIETSYVK	278	8	-0.0004	0.0027				478
LLGDNQVMPK	189	10	0.0093	0.0014				479
LLLKYRAR	120	8	-0.0009	-0.0004				480
LSMLEVFEGR	225	10	-0.0004	0.0001				481
LVHFLLLK	116	8	0.0290	0.1500	0.0007	-0.0009	0.0200	482
LVHFLLLKYR	116	10	0.0260	0.0022				483
LVQENYLEYR	250	10	0.0027	0.0089				484
MLEVFEGR	227	8	-0.0009	-0.0004				485
MVELVHFLLLK	113	11	0.0200	0.0120	0.0038	0.0056	0.0220	486
PACYEFLWGPR	266	11	-0.0009	-0.0002				487
PLEQRSQHCK	2	10	0.0003	0.0002				488
PLHERALR	303	8	-0.0009	-0.0004				489
RALIETSYVK	276	10	0.0200	0.0750	0.0064	0.0003	0.0026	490
RAREPVTK	125	8	-0.0009	-0.0003				491
SMLEVFEGR	226	9	0.0020	0.0220	0.4900	3.2000	0.0044	492
SSNQEEEGPR	87	10	0.0002	0.0002				493
STTINYTLWR	72	10	0.0014	0.0910				494
SVFAHPRK	237	8	0.1410	0.0810	0.0130	0.0010	0.0440	495
TINYTLWR	74	8	0.0140	0.0550	0.0250	0.0370	0.3800	496
TTINYTLWR	73	9	0.0890	1.1000				497
YVKVLHHTLK	283	10	0.0033	0.0160	0.0005	-0.0009	0.0360	498

Table IX B

Mage 3 A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
ALVETSYVK	277	9	0.0270	0.1700	0.0009	0.0004	0.0022	499
DSILGDPK	236	8	-0.0004	-0.0003				500
DSILGDPKK	236	9	-0.0003	-0.0002				501
ELSVLEVFEGR	224	11	-0.0009	0.0023				502
ELVHFLLLK	115	9	0.0045	0.0011				503
ELVHFLLLKYR	115	11	0.0011	0.0031				504
ESEFQAALSR	102	10	0.0002	0.0002				505
ESEFQAALSRK	102	11	0.0002	0.0004				506
FLLLKYRAR	119	9						507
FVQENYLEYR	250	10	0.0009	0.0012				508
GLLGDNQIMPK	188	11	0.1300	0.0570	-0.0006	-0.0013	-0.0001	509
IIVLAIIAR	203	9	0.0069	0.0011				510
IVLAIIAR	204	8	0.0053	0.0037				511
KVLHHMVK	285	8	0.0580	0.0190	0.0012	0.0052	-0.0001	512
LIIVLAIIAR	202	10	0.0280	0.0021				513
LLGDNQIMPK	189	10	0.0200	0.0110				514
LLIIVLAIIAR	201	11	0.0021	0.0056				515
LLLKYRAR	120	8	-0.0009	-0.0004				516
LSVLEVFEGR	225	10	-0.0006	0.0030				517
LVETSYVK	278	8	-0.0004	0.0014				518
LVHFLLLK	116	8	0.0290	0.1500	0.0007	-0.0009	0.0200	519
LVHFLLLKYR	116	10	0.0260	0.0022				520
PACYEFLWGPR	266	11	-0.0009	-0.0002				521
PLEQRSQHCK	2	10	0.0003	0.0002				522
PLHEWVLR	303	8	-0.0009	-0.0003				523
RALVETSYVK	276	10	0.0190	0.1100	0.0034	0.0003	0.0004	524
RAREPVTK	125	8	-0.0009	-0.0003				525
SILGDPKK	237	8	-0.0009	0.0012				526
SVLEVFEGR	226	9	0.0003	0.1400	0.1700	0.6600	0.0860	527
VAELVHFLLLK	113	11	-0.0002	0.0011				528
VLEVFEGR	227	8	0.0016	0.0005				529
YVKVLHHMVK	283	10	0.0020	0.0061				530

Table X A
Mage 2 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
AISRKMVEL	108	9		531
ALIETSYVKVL	277	11		532
CLGLSYDGL	181	9		533
CLGLSYDGLL	181	10		534
CYEFLWGPRAL	268	11	0.0004	535
DLESEFQAAI	100	10		536
DLVQENYL	249	8		537
DLVQENYLEY	249	10		538
EFLWGPRAL	270	9	0.0006	539
EFLWGPRALI	270	10	0.0097	540
EFQAAISRKM	104	10	0.0002	541
ELSMLEVF	224	8		542
ELVHFLLL	115	8		543
ELVHFLLLKY	115	10		544
ETSYVKVL	280	8		545
EVFEGREDSVF	229	11		546
EVVEVVPI	165	8		547
EVVEVVPISHL	165	11		548
EVVPISHL	168	8		549
EVVPISHLY	168	9		550
EVVPISHLYI	168	10		551
EVVPISHLYIL	168	11		552
EYLQLVFGI	156	9	3.5000	553
FLWGPRAL	271	8		554
FLWGPRALI	271	9		555
GIEVVEVVPI	163	10		556
GLEARGEAL	15	9		557
GLEARGEALGL	15	11		558
GLLGDNQVM	188	9		559
GLLIIVLAI	200	9		560
GLLIIVLAII	200	10		561
GLSYDGLL	183	8		562
HLYILVTCL	174	9		563
HLYILVTCLGL	174	11		564
HTLKIGGEPHI	289	11		565
IFSKASEY	150	8		566
IFSKASEYL	150	9	0.0230	567
IFSKASEYLQL	150	11	0.0950	568
IIVLAIIAI	203	9		569
ILVTCLGL	177	8		570
ILVTCLGLSY	177	10		571
IVLAIIAI	204	8		572
IWEELSML	221	8	0.0007	573
IWEELSMLEVF	221	11	0.0170	574
KIGGEPHI	292	8		575
KIGGEPHISY	292	10		576

Table X A

Mage 2_A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
KIWEELSM	220	8		577
KIWEELSML	220	9		578
KMVELVHF	112	8	0.0005	579
KMVELVHFL	112	9		580
KMVELVHFLL	112	10		581
KMVELVHFLLL	112	11		582
KTGLLIIVL	198	9		583
KTGLLIIVLAI	198	11		584
KVLHHTLKI	285	9		585
LIETSYVKVL	278	10		586
LIIVLAII	202	8		587
LIIVLAIIAI	202	10		588
LLGDNQVM	189	8		589
LLIIVLAI	201	8		590
LLIIVLAII	201	9		591
LLIIVLAIIAI	201	11		592
LLMQDLVQENY	245	11		593
LMQDLVQENY	246	10		594
LMQDLVQENYL	246	11		595
LVHFLLLKY	116	9		596
LVQENYLEY	250	9		597
LVTCLGLSY	178	9		598
LWGPRALI	272	8	0.1200	599
LYILVTCL	175	8	0.0086	600
LYILVTCLGL	175	10	0.0140	601
MFPDLESEF	97	9	0.0140	602
MVELVHFL	113	8		603
MVELVHFLL	113	9		604
MVELVHFLLL	113	10		605
PISHLYIL	171	8		606
PVIFSKASEY	148	10		607
PVIFSKASEYL	148	11		608
PVTKAEML	129	8		609
QTASSSSTL	37	9		610
QVMPKTGL	194	8		611
QVMPKTGLL	194	9		612
QVMPKTGLLI	194	10		613
QVMPKTGLLII	194	11		614
QVPGSDPACY	260	10		615
RMFPDLESEF	96	10	0.0016	616
SFSTTINY	70	8		617
SFSTTINYTL	70	10	0.0150	618
SFSTTINYTLW	70	11	0.0280	619
STLVEVTL	43	8		620
STTINYTL	72	8		621
STTINYTLW	72	9		622

Table X A
Mage 2 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
SVFAHPRKL	237	9		623
SVFAHPRKLL	237	10		624
SVFAHPRKLLM	237	11		625
SVLRNCQDF	138	9		626
SVLRNCQDFF	138	10		627
SYPPLHERAL	300	10	0.0003	628
SYVKVLHHTL	282	10	0.1600	629
TLKIGGEPHI	290	10		630
TTINYTLW	73	8		631
VFAHPRKL	238	8	0.0005	632
VFAHPRKLL	238	9	0.0006	633
VFAHPRKLLM	238	10		634
VFEGREDSVF	230	10	0.0004	635
VIFSKASEY	149	9		636
VIFSKASEYL	149	10		637
VLHHTLKI	286	8		638
VLRNCQDF	139	8		639
VLRNCQDFF	139	9		640
VMPKTGLL	195	8	-0.0004	641
VMPKTGLLI	195	9	0.2300	642
VMPKTGLLII	195	10	0.0580	643
VTCLGLSY	179	8		644
VTCLGLSYDGL	179	11		645
VTKAEMLESVL	130	11		646
VVEVVPISHL	166	10		647
VVEVVPISHLY	166	11		648
VVPISHLY	169	8		649
VVPISHLYI	169	9		650
VVPISHLYIL	169	10		651
YILVTCLGL	176	9		652
YILVTCLGLSY	176	11		653
YLQLVFGI	157	8		654
YVKVLHHTL	283	9		655
YVKVLHHTLKI	283	11		656

Table X B

Mage 3 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
ALSRKVAEL	108	9		657
ALVETSYVKVL	277	11		658
ATCLGLSY	179	8		659
ATCLGLSYDGL	179	11		660
CLGLSYDGL	181	9		661
CLGLSYDGLL	181	10		662
CYEFLWGPRAL	268	11	0.0004	663
DLESEFQAAL	100	10		664
EFLWGPRAL	270	9	0.0006	665
ELMEVDPI	165	8		666
ELMEVDPIGHL	165	11		667
ELSVLEVF	224	8		668
ELVHFLLL	115	8		669
ELVHFLLLKY	115	10		670
EMLGSVVGNW	134	10	0.0017	671
ETSYVKVL	280	8		672
ETSYVKVLHHM	280	11		673
EVDPIGHL	168	8		674
EVDPIGHLY	168	9		675
EVDPIGHLYI	168	10		676
EVDPIGHLYIF	168	11		677
EVFEGREDSI	229	10		678
EVFEGREDSIL	229	11		679
FLWGPRAL	271	8		680
FVQENYLEY	250	9		681
GIELMEVDPI	163	10		682
GLEARGEAL	15	9		683
GLEARGEALGL	15	11		684
GLLGDNQI	188	8		685
GLLGDNQIM	188	9		686
GLLIIVLAI	200	9		687
GLLIIVLAII	200	10		688
GLSYDGLL	183	8		689
HFVQENYL	249	8	-0.0004	690
HFVQENYLEY	249	10		691
HISYPPLHEW	298	10		692
HLYIFATCL	174	9		693
HLYIFATCLGL	174	11		694
HMVKISGGPHI	289	11		695
IFATCLGL	177	8	0.0120	696
IFATCLGLSY	177	10		697
IFSKASSSL	150	9	0.0160	698
IFSKASSSLQL	150	11	0.0910	699
ILGDPKKL	238	8		700
ILGDPKKLL	238	9		701

Table X B

Mage 3 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
IMPKAGLL	195	8		702
IMPKAGLLI	195	9	0.4200	703
IMPKAGLLII	195	10	0.0500	704
IWEELSVL	221	8	-0.0004	705
IWEELSVLEVF	221	11	0.0260	706
KISGGPHI	292	8		707
KISGGPHISY	292	10		708
KIWEELSVL	220	9		709
KVAELVHF	112	8		710
KVAELVHFL	112	9		711
KVAELVHFLL	112	10		712
KVAELVHFLLL	112	11		713
KVLHHMVKI	285	9		714
LIIVLAII	202	8		715
LLGDNQIM	189	8		716
LLIIVLAI	201	8		717
LLIIVLAII	201	9		718
LLTQHFVQENY	245	11		719
LMEVDPIGHL	166	10		720
LMEVDPIGHLY	166	11		721
LTQHFVQENY	246	10		722
LTQHFVQENYL	246	11		723
LVETSYVKVL	278	10		724
LVFGIELM	160	8		725
LVHFLLLKY	116	9		726
LYIFATCL	175	8	0.0140	727
LYIFATCLGL	175	10	0.0480	728
MLGSVVGNW	135	9		729
MLGSVVGNWQY	135	11		730
MVKISGGPHI	290	10		731
NWQYFFPVI	142	9	0.5300	732
NWQYFFPVIF	142	10	0.0170	733
NYPLWSQSY	76	9	0.0270	734
PIGHLYIF	171	8		735
PTTMNYPL	72	8		736
PTTMNYPLW	72	9		737
PVIFSKASSSL	148	11		738
PVTKAEML	129	8		739
QIMPKAGL	194	8		740
QIMPKAGLL	194	9		741
QIMPKAGLLI	194	10		742
QIMPKAGLLII	194	11		743
QLVFGIEL	159	8		744
QLVFGIELM	159	9		745
QVPGSDPACY	260	10		746

Table X B

Mage 3 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
QYFFPVIF	144	8	0.1200	747
SILGDPKKL	237	9		748
SILGDPKKLL	237	10		749
SLPTTMNY	70	8		750
SLPTTMNYPL	70	10		751
SLPTTMNYPLW	70	11		752
SLQLVFGI	157	8		753
SLQLVFGIEL	157	10		754
SLQLVFGIELM	157	11		755
STFPDLESEF	96	10		756
STLVEVTL	43	8		757
SVVGNWQY	138	8		758
SVVGNWQYF	138	9		759
SVVGNWQYFF	138	10		760
SYDGLLGDNQI	185	11	0.0026	761
SYPPLHEW	300	8	0.0420	762
SYPPLHEWVL	300	10	0.5900	763
SYVKVLHHM	282	9		764
TFPDLESEF	97	9	0.0049	765
TMNYPLWSQSY	74	11		766
TTMNYPLW	73	8		767
VFEGREDSI	230	9	-0.0004	768
VFEGREDSIL	230	10	-0.0005	769
VIFSKASSSL	149	10		770
VLHHMVKI	286	8		771
VVGNWQYF	139	8		772
VVGNWQYFF	139	9		773
YIFATCLGL	176	9		774
YIFATCLGLSY	176	11		775
YVKVLHHM	283	8		776
YVKVLHHMVKI	283	11		777

Table XI A
Mage 2 B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
APATEEQQTA	30	10	0.0002	778
APEEKIWEEL	216	10	0.0001	779
DPACYEFL	265	8	-0.0002	780
DPACYEFLW	265	9	0.0001	781
EPHISYPPL	296	9	0.1100	782
EPVTKAEM	128	8	0.0010	783
EPVTKAEML	128	9	0.0001	784
FPDLESEF	98	8	-0.0002	785
FPDLESEFQA	98	10	0.0002	786
FPDLESEFQAA	98	11	-0.0001	787
FPVIFSKA	147	8	0.0003	788
FPVIFSKASEY	147	11	0.0004	789
GPRALIETSY	274	10	0.0008	790
GPRALIETSYV	274	11	0.1300	791
GPRMFPDL	94	8	0.0063	792
HPRKLLMQDL	241	10	0.0400	793
HPRKLLMQDLV	241	11	0.0042	794
KPEEGLEA	11	8	-0.0002	795
MPKTGLLI	196	8	0.0190	796
MPKTGLLII	196	9	0.0020	797
MPKTGLLIIV	196	10	0.0003	798
MPKTGLLIIVL	196	11	0.0099	799
PPHSPQGA	61	8	-0.0002	800
PPHSPQGASSF	61	11	-0.0003	801
PPLHERAL	302	8	0.0026	802
SPPHSPQGA	60	9	0.0001	803
SPQGASSF	64	8	0.0007	804
SPSPPHSPQGA	58	11	0.0006	805
VPGSDPACY	261	9	0.0001	806
VPGSDPACYEF	261	11	-0.0001	807
VPISHLYI	170	8	0.0170	808
VPISHLYIL	170	9	0.2500	809
VPISHLYILV	170	10	0.0027	810
YPPLHERA	301	8	-0.0002	811
YPPLHERAL	301	9	0.2700	812

Table XI B

Mage 3 B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
APATEEQEA	30	9	0.0001	813
APATEEQEAA	30	10	0.0002	814
APEEKIWEEL	216	10	0.0001	815
DPACYEFL	265	8	-0.0002	816
DPACYEFLW	265	9	0.0001	817
DPIGHLYI	170	8	-0.0002	818
DPIGHLYIF	170	9	0.0001	819
DPIGHLYIFA	170	10	0.0002	820
DPKKLLTQHF	241	10	0.0001	821
DPKKLLTQHFV	241	11	-0.0004	822
DPPQSPQGA	60	9	0.0001	823
EPVTKAEM	128	8	0.0010	824
EPVTKAEML	128	9	0.0001	825
FPDLESEF	98	8	-0.0002	826
FPDLESEFQA	98	10	0.0002	827
FPDLESEFQAA	98	11	-0.0001	828
FPVIFSKA	147	8	0.0003	829
GPHISYPPL	296	9	0.8800	830
GPRALVETSY	274	10	0.0002	831
GPRALVETSYV	274	11	0.1900	832
GPSTFPDL	94	8	-0.0002	833
KPEEGLEA	11	8	-0.0002	834
LPTTMNYPL	71	9	0.0770	835
LPTTMNYPLW	71	10	0.0001	836
MPKAGLLI	196	8	0.1300	837
MPKAGLLII	196	9	0.0170	838
MPKAGLLIIV	196	10	0.0031	839
MPKAGLLIIVL	196	11	0.0280	840
PPLHEWVL	302	8	-0.0002	841
PPQSPQGA	61	8	-0.0002	842
PPQSPQGASSL	61	11	0.0049	843
SPDPPQSPQGA	58	11	-0.0001	844
SPQGASSL	64	8	0.0081	845
VPGSDPACY	261	9	0.0001	846
VPGSDPACYEF	261	11	-0.0001	847
YPLWSQSY	77	8	-0.0002	848
YPPLHEWV	301	8	-0.0002	849
YPPLHEWVL	301	9	0.0027	850

Table XII A

Mage 2 B27 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AHPRKLLM	240	8	851
AHPRKLLMQDL	240	11	852
AREPVTKAEM	126	10	853
AREPVTKAEML	126	11	854
ARGEALGL	18	8	855
EKIWEELSM	219	9	856
EKIWEELSML	219	10	857
LKIGGEPHI	291	9	858
LKIGGEPHISY	291	11	859
LRNCQDFF	140	8	860
LRNCQDFFPVI	140	11	861
PHISYPPL	297	8	862
PHSPQGASSF	62	10	863
PKTGLLII	197	8	864
PKTGLLIIVL	197	10	865
PRALIETSY	275	9	866
PRKLLMQDL	242	9	867
PRMFPDLESEF	95	11	868
QHCKPEEGL	8	9	869
RKLLMQDL	243	8	870
RKMVELVHF	111	9	871
RKMVELVHFL	111	10	872
RKMVELVHFLL	111	11	873
SHLYILVTCL	173	10	874
SKASEYLQL	152	9	875
SKASEYLQLVF	152	11	876
SRKMVELVHF	110	10	877
SRKMVELVHFL	110	11	878
TKAEMLESVL	131	10	879
VHFLLLKY	117	8	880
VKVLHHTL	284	8	881
VKVLHHTLKI	284	10	882

Table XII B

Mage 3 B27 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AREPVTKAEM	126	10	883
AREPVTKAEML	126	11	884
ARGEALGL	18	8	885
EKIWEELSVL	219	10	886
GHLYIFATCL	173	10	887
KKLLTQHF	243	8	888
PHISYPPL	297	8	889
PHISYPPLHEW	297	11	890
PKAGLLII	197	8	891
PKAGLLIIVL	197	10	892
PKKLLTQHF	242	9	893
PRALVETSY	275	9	894
QHCKPEEGL	8	9	895
QHFVQENY	248	8	896
QHFVQENYL	248	9	897
QHFVQENYLEY	248	11	898
RKVAELVHF	111	9	899
RKVAELVHFL	111	10	900
RKVAELVHFLL	111	11	901
SKASSSLQL	152	9	902
SKASSSLQLVF	152	11	903
SRKVAELVHF	110	10	904
SRKVAELVHFL	110	11	905
VHFLLLKY	117	8	906
VKISGGPHI	291	9	907
VKISGGPHISY	291	11	908
VKVLHHMVKI	284	10	909

Table XIII A
Mage 2 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AAISRKMV	107	8	910
AAISRKMVEL	107	10	911
AAISRKMVELV	107	11	912
ASEYLQLV	154	8	913
ASEYLQLVF	154	9	914
ASEYLQLVFGI	154	11	915
ASSFSTTI	68	8	916
ASSFSTTINY	68	10	917
ASSSSTLV	39	8	918
ASSSSTLVEV	39	10	919
CAPEEKIW	215	8	920
CAPEEKIWEEL	215	11	921
DSVFAHPRKL	236	10	922
DSVFAHPRKLL	236	11	923
EARGEALGL	17	9	924
EARGEALGLV	17	10	925
ESEFQAAI	102	8	926
ESVLRNCQDF	137	10	927
ESVLRNCQDFF	137	11	928
ETSYVKVL	280	8	929
FAHPRKLL	239	8	930
FAHPRKLLM	239	9	931
FSKASEYL	151	8	932
FSKASEYLQL	151	10	933
FSKASEYLQLV	151	11	934
FSTTINYTL	71	9	935
FSTTINYTLW	71	10	936
GASSFSTTI	67	9	937
GASSFSTTINY	67	11	938
GSDPACYEF	263	9	939
GSDPACYEFL	263	10	940
GSDPACYEFLW	263	11	941
HSPQGASSF	63	9	942
HTLKIGGEPHI	289	11	943
ISHLYILV	172	8	944
ISHLYILVTCL	172	11	945
ISRKMVEL	109	8	946
ISRKMVELV	109	9	947
ISRKMVELVHF	109	11	948
ISYPPLHERAL	299	11	949
KAEMLESV	132	8	950
KAEMLESVL	132	9	951
KASEYLQL	153	8	952
KASEYLQLV	153	9	953
KASEYLQLVF	153	10	954
KTGLLIIV	198	8	955

Table XIII A
Mage 2 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
KTGLLIIVL	198	9	956
KTGLLIIVLAI	198	11	957
PACYEFLW	266	8	958
QAAISRKM	106	8	959
QAAISRKMV	106	9	960
QAAISRKMVEL	106	11	961
QTASSSSTL	37	9	962
QTASSSSTLV	37	10	963
RALIETSY	276	8	964
RALIETSYV	276	9	965
RALIETSYVKV	276	11	966
RAREPVTKAEM	125	11	967
RSQHCKPEEGL	6	11	968
SSFSTTINY	69	9	969
SSFSTTINYTL	69	11	970
SSNQEEEGPRM	87	11	971
SSSSTLVEV	40	9	972
SSSSTLVEVTL	40	11	973
SSSTLVEV	41	8	974
SSSTLVEVTL	41	10	975
SSTLVEVTL	42	9	976
STLVEVTL	43	8	977
STLVEVTLGEV	43	11	978
STTINYTL	72	8	979
STTINYTLW	72	9	980
TASSSSTL	38	8	981
TASSSSTLV	38	9	982
TASSSSTLVEV	38	11	983
TSYVKVLHHTL	281	11	984
TTINYTLW	73	8	985
VTCLGLSY	179	8	986
VTCLGLSYDGL	179	11	987
VTKAEMLESV	130	10	988
VTKAEMLESVL	130	11	989

Table XIII B

Mage 3 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AALSRKVAEL	107	10	990
AALSRKVAELV	107	11	991
AASSSSTL	38	8	992
AASSSSTLV	38	9	993
AASSSSTLVEV	38	11	994
ASSLPTTM	68	8	995
ASSLPTTMNY	68	10	996
ASSSLQLV	154	8	997
ASSSLQLVF	154	9	998
ASSSLQLVFGI	154	11	999
ASSSSTLV	39	8	1000
ASSSSTLVEV	39	10	1001
ATCLGLSY	179	8	1002
ATCLGLSYDGL	179	11	1003
CAPEEKIW	215	8	1004
CAPEEKIWEEL	215	11	1005
DSILGDPKKL	236	10	1006
DSILGDPKKLL	236	11	1007
EAASSSSTL	37	9	1008
EAASSSSTLV	37	10	1009
EARGEALGL	17	9	1010
EARGEALGLV	17	10	1011
ESEFQAAL	102	8	1012
ETSYVKVL	280	8	1013
ETSYVKVLHHM	280	11	1014
FATCLGLSY	178	9	1015
FSKASSSL	151	8	1016
FSKASSSLQL	151	10	1017
FSKASSSLQLV	151	11	1018
GASSLPTTM	67	9	1019
GASSLPTTMNY	67	11	1020
GSDPACYEF	263	9	1021
GSDPACYEFL	263	10	1022
GSDPACYEFLW	263	11	1023
GSVVGNWQY	137	9	1024
GSVVGNWQYF	137	10	1025
GSVVGNWQYFF	137	11	1026
ISGGPHISY	293	9	1027
ISYPPLHEW	299	9	1028
ISYPPLHEWV	299	10	1029
ISYPPLHEWVL	299	11	1030
KAEMLGSV	132	8	1031
KAEMLGSVV	132	9	1032
KAGLLIIV	198	8	1033
KAGLLIIVL	198	9	1034
KAGLLIIVLAI	198	11	1035

Table XIII B

Mage 3 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
KASSSLQL	153	8	1036
KASSSLQLV	153	9	1037
KASSSLQLVF	153	10	1038
LSRKVAEL	109	8	1039
LSRKVAELV	109	9	1040
LSRKVAELVHF	109	11	1041
LTQHFVQENY	246	10	1042
LTQHFVQENYL	246	11	1043
PACYEFLW	266	8	1044
PSTFPDLESEF	95	11	1045
PTTMNYPL	72	8	1046
PTTMNYPLW	72	9	1047
QAALSRKV	106	8	1048
QAALSRKVAEL	106	11	1049
QSPQGASSL	63	9	1050
RALVETSY	276	8	1051
RALVETSYV	276	9	1052
RALVETSYVKV	276	11	1053
RAREPVTKAEM	125	11	1054
RSQHCKPEEGL	6	11	1055
SSLPTTMNY	69	9	1056
SSLPTTMNYPL	69	11	1057
SSLQLVFGI	156	9	1058
SSLQLVFGIEL	156	11	1059
SSSLQLVF	155	8	1060
SSSLQLVFGI	155	10	1061
SSSSTLVEV	40	9	1062
SSSSTLVEVTL	40	11	1063
SSSTLVEV	41	8	1064
SSSTLVEVTL	41	10	1065
SSTLVEVTL	42	9	1066
STFPDLESEF	96	10	1067
STLVEVTL	43	8	1068
STLVEVTLGEV	43	11	1069
TSYVKVLHHM	281	10	1070
TSYVKVLHHMV	281	11	1071
TTMNYPLW	73	8	1072
VAELVHFL	113	8	1073
VAELVHFLL	113	9	1074
VAELVHFLLL	113	10	1075
VTKAEMLGSV	130	10	1076
VTKAEMLGSVV	130	11	1077

Table XIV A
Mage 2 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AISRKMVELV	108	10	1078
ALIETSYV	277	8	1079
ALIETSYVKV	277	10	1080
CQDFFPVI	143	8	1081
CQDFFPVIF	143	9	1082
DLESEFQAAI	100	10	1083
DLVQENYLEY	249	10	1084
DPACYEFLW	265	9	1085
ELSMLEVF	224	8	1086
ELVHFLLLKY	115	10	1087
EPVTKAEM	128	8	1088
EVFEGREDSV	229	10	1089
EVFEGREDSVF	229	11	1090
EVVEVVPI	165	8	1091
EVVPISHLY	168	9	1092
EVVPISHLYI	168	10	1093
FLWGPRALI	271	9	1094
FPDLESEF	98	8	1095
FPVIFSKASEY	147	11	1096
FQAAISRKM	105	9	1097
FQAAISRKMV	105	10	1098
GIEVVEVV	163	8	1099
GIEVVEVVPI	163	10	1100
GLLGDNQV	188	8	1101
GLLGDNQVM	188	9	1102
GLLIIVLAI	200	9	1103
GLLIIVLAII	200	10	1104
GPRALIETSY	274	10	1105
GPRALIETSYV	274	11	1106
HPRKLLMQDLV	241	11	1107
IIVLAIIAI	203	9	1108
ILVTCLGLSY	177	10	1109
IVLAIIAI	204	8	1110
KIGGEPHI	292	8	1111
KIGGEPHISY	292	10	1112
KIWEELSM	220	8	1113
KIWEELSMLEV	220	11	1114
KLLMQDLV	244	8	1115
KMVELVHF	112	8	1116
KVLHHTLKI	285	9	1117
LIETSYVKV	278	9	1118
LIIVLAII	202	8	1119
LIIVLAIIAI	202	10	1120
LLGDNQVM	189	8	1121
LLIIVLAI	201	8	1122
LLIIVLAII	201	9	1123

Table XIV A
Mage 2 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
LLIIVLAIIAI	201	11	1124
LLKYRAREPV	121	10	1125
LLLKYRAREPV	120	11	1126
LLMQDLVQENY	245	11	1127
LMQDLVQENY	246	10	1128
LQLVFGIEV	158	9	1129
LQLVFGIEVV	158	10	1130
LVEVTLGEV	45	9	1131
LVFGIEVV	160	8	1132
LVFGIEVVEV	160	10	1133
LVFGIEVVEVV	160	11	1134
LVHFLLLKY	116	9	1135
LVQENYLEY	250	9	1136
LVTCLGLSY	178	9	1137
MPKTGLLI	196	8	1138
MPKTGLLII	196	9	1139
MPKTGLLIIV	196	10	1140
MQDLVQENY	247	9	1141
NQEEEGPRM	89	9	1142
NQEEEGPRMF	89	10	1143
NQVMPKTGLLI	193	11	1144
PISHLYILV	171	9	1145
PPHSPQGASSF	61	11	1146
PQGASSFSTTI	65	11	1147
PVIFSKASEY	148	10	1148
PVTKAEMLESV	129	11	1149
QLVFGIEV	159	8	1150
QLVFGIEVV	159	9	1151
QLVFGIEVVEV	159	11	1152
QQTASSSSTLV	36	11	1153
QVMPKTGLLI	194	10	1154
QVMPKTGLLII	194	11	1155
QVPGSDPACY	260	10	1156
RMFPDLESEF	96	10	1157
RQVPGSDPACY	259	11	1158
SPQGASSF	64	8	1159
SVFAHPRKLLM	237	11	1160
SVLRNCQDF	138	9	1161
SVLRNCQDFF	138	10	1162
TLKIGGEPHI	290	10	1163
TLVEVTLGEV	44	10	1164
VIFSKASEY	149	9	1165
VLHHTLKI	286	8	1166
VLRNCQDF	139	8	1167
VLRNCQDFF	139	9	1168
VLRNCQDFFPV	139	11	1169

Table XIV A

Mage 2 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
VMPKTGLLI	195	9	1170
VMPKTGLLII	195	10	1171
VMPKTGLLIIV	195	11	1172
VPGSDPACY	261	9	1173
VPGSDPACYEF	261	11	1174
VPISHLYI	170	8	1175
VPISHLYILV	170	10	1176
VQENYLEY	251	8	1177
VQENYLEYRQV	251	11	1178
VVEVVPISHLY	166	11	1179
VVPISHLY	169	8	1180
VVPISHLYI	169	9	1181
VVPISHLYILV	169	11	1182
YILVTCLGLSY	176	11	1183
YLQLVFGI	157	8	1184
YLQLVFGIEV	157	10	1185
YLQLVFGIEVV	157	11	1186
YVKVLHHTLKI	283	11	1187

Table XIV B
Mage 3 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
ALSRKVAELV	108	10	1188
ALVETSYV	277	8	1189
ALVETSYVKV	277	10	1190
DPACYEFLW	265	9	1191
DPIGHLYI	170	8	1192
DPIGHLYIF	170	9	1193
DPKKLLTQHF	241	10	1194
DPKKLLTQHFV	241	11	1195
ELMEVDPI	165	8	1196
ELSVLEVF	224	8	1197
ELVHFLLLKY	115	10	1198
EMLGSVVGNW	134	10	1199
EPVTKAEM	128	8	1200
EVDPIGHLY	168	9	1201
EVDPIGHLYI	168	10	1202
EVDPIGHLYIF	168	11	1203
EVFEGREDSI	229	10	1204
FLWGPRALV	271	9	1205
FPDLESEF	98	8	1206
FQAALSRKV	105	9	1207
FVQENYLEY	250	9	1208
GIELMEVDPI	163	10	1209
GLLGDNQI	188	8	1210
GLLGDNQIM	188	9	1211
GLLIIVLAI	200	9	1212
GLLIIVLAII	200	10	1213
GPRALVETSY	274	10	1214
GPRALVETSYV	274	11	1215
HISYPPLHEW	298	10	1216
HISYPPLHEWV	298	11	1217
HMVKISGGPHI	289	11	1218
IMPKAGLLI	195	9	1219
IMPKAGLLII	195	10	1220
IMPKAGLLIIV	195	11	1221
KISGGPHI	292	8	1222
KISGGPHISY	292	10	1223
KIWEELSV	220	8	1224
KIWEELSVLEV	220	11	1225
KLLTQHFV	244	8	1226
KVAELVHF	112	8	1227
KVLHHMVKI	285	9	1228
LIIVLAII	202	8	1229
LLGDNQIM	189	8	1230
LLIIVLAI	201	8	1231
LLIIVLAII	201	9	1232
LLKYRAREPV	121	10	1233

Table XIV B

Mage 3 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
LLLKYRAREPV	120	11	1234
LLTQHFVQENY	245	11	1235
LMEVDPIGHLY	166	11	1236
LPTTMNYPLW	71	10	1237
LQLVFGIELM	158	10	1238
LVETSYVKV	278	9	1239
LVEVTLGEV	45	9	1240
LVFGIELM	160	8	1241
LVFGIELMEV	160	10	1242
LVHFLLLKY	116	9	1243
MLGSVVGNW	135	9	1244
MLGSVVGNWQY	135	11	1245
MPKAGLLI	196	8	1246
MPKAGLLII	196	9	1247
MPKAGLLIIV	196	10	1248
MVKISGGPHI	290	10	1249
NQEEEGPSTF	89	10	1250
NQIMPKAGLLI	193	11	1251
PIGHLYIF	171	8	1252
PQGASSLPTTM	65	11	1253
PVTKAEMLGSV	129	11	1254
QIMPKAGLLI	194	10	1255
QIMPKAGLLII	194	11	1256
QLVFGIELM	159	9	1257
QLVFGIELMEV	159	11	1258
QVPGSDPACY	260	10	1259
RQVPGSDPACY	259	11	1260
SLPTTMNY	70	8	1261
SLPTTMNYPLW	70	11	1262
SLQLVFGI	157	8	1263
SLQLVFGIELM	157	11	1264
SVVGNWQY	138	8	1265
SVVGNWQYF	138	9	1266
SVVGNWQYFF	138	10	1267
TLVEVTLGEV	44	10	1268
TMNYPLWSQSY	74	11	1269
TQHFVQENY	247	9	1270
VLHHMVKI	286	8	1271
VPGSDPACY	261	9	1272
VPGSDPACYEF	261	11	1273
VQENYLEY	251	8	1274
VQENYLEYRQV	251	11	1275
VVGNWQYF	139	8	1276
VVGNWQYFF	139	9	1277
VVGNWQYFFPV	139	11	1278
WQYFFPVI	143	8	1279

Table XIV B

Mage 3 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
WQYFFPVIF	143	9	1280
YIFATCLGLSY	176	11	1281
YPLWSQSY	77	8	1282
YPPLHEWV	301	8	1283
YVKVLHHM	283	8	1284
YVKVLHHMV	283	9	1285
YVKVLHHMVKI	283	11	1286

Table XV A
Mage 2 A01 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASSFSTTINY	68	10	0.1700	1287
GASSFSTTINY	67	11	0.0047	1288
GGEPHISY	294	8	-0.0021	1289
IFSKASEY	150	8	0.0023	1290
LMQDLVQENY	246	10	0.0450	1291
MQDLVQENY	247	9	1.5000	1292
PGSDPACY	262	8	-0.0021	1293
PRALIETSY	275	9	-0.0006	1294
SFSTTINY	70	8	-0.0021	1295
SSFSTTINY	69	9	0.0430	1296
VQENYLEY	251	8	-0.0021	1297
VTCLGLSY	179	8		1298
VVEVVPISHLY	166	11	0.2000	1299

Table XV B

Mage 3 A01 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASSLPTTMNY	68	10	2.6000	1300
ATCLGLSY	179	8	0.1100	1301
EVDPIGHLY	168	9	18.0000	1302
GASSLPTTMNY	67	11	0.0390	1303
GSVVGNWQY	137	9	0.0500	1304
IFATCLGLSY	177	10	0.0020	1305
ISGGPHISY	293	9	0.0370	1306
KISGGPHISY	292	10	0.0011	1307
LGSVVGNWQY	136	10	0.0020	1308
LMEVDPIGHLY	166	11	7.5000	1309
LTQHFVQENY	246	10	0.2600	1310
PGSDPACY	262	8	-0.0021	1311
PRALVETSY	275	9	0.0011	1312
SSLPTTMNY	69	9	0.0550	1313
TMNYPLWSQSY	74	11	0.0830	1314
VQENYLEY	251	8	-0.0021	1315

Table XVI A
Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
AADSPSPPH	55	9	0.0003	1316
ACYEFLWGPR	267	10	0.0032	1317
ACYEFLWGPRA	267	11		1318
ADSPSPPH	56	8		1319
AIEGDCAPEEK	210	11	0.0009	1320
AIIAIEGDCA	207	10		1321
AISRKMVELVH	108	11		1322
ALGLVGAQA	22	9	0.0003	1323
ALGLVGAQAPA	22	11		1324
ALIETSYVK	277	9	0.0810	1325
ASEYLQLVF	154	9	0.0002	1326
ASSFSTTINY	68	10	0.0009	1327
ATEEQQTA	32	8		1328
DFFPVIFSK	145	9	0.0002	1329
DFFPVIFSKA	145	10		1330
DLESEFQA	100	8		1331
DLESEFQAA	100	9		1332
DLVQENYLEY	249	10		1333
DLVQENYLEYR	249	11	0.0047	1334
DSVFAHPR	236	8	-0.0004	1335
DSVFAHPRK	236	9	0.0021	1336
EALGLVGA	21	8		1337
EALGLVGAQA	21	10	0.0003	1338
EDSVFAHPR	235	9		1339
EDSVFAHPRK	235	10		1340
EFLWGPRA	270	8		1341
EFQAAISR	104	8		1342
EFQAAISRK	104	9	0.0002	1343
EGDCAPEEK	212	9	0.0002	1344
EGLEARGEA	14	9	0.0003	1345
EGREDSVF	232	8		1346
EGREDSVFA	232	9		1347
EGREDSVFAH	232	10		1348
ELSMLEVF	224	8		1349
ELSMLEVFEGR	224	11	0.0016	1350
ELVHFLLLK	115	9	0.0045	1351
ELVHFLLLKY	115	10	0.0066	1352
ELVHFLLLKYR	115	11	0.0011	1353
EMLESVLR	134	8	-0.0009	1354
ESEFQAAISR	102	10	0.0002	1355
ESEFQAAISRK	102	11	0.0010	1356
ESVLRNCQDF	137	10	0.0002	1357
ESVLRNCQDFF	137	11		1358
ETSYVKVLH	280	9		1359
ETSYVKVLHH	280	10		1360
EVFEGREDSVF	229	11		1361

Table XVI A

Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
EVTLGEVPA	47	9	0.0003	1362
EVTLGEVPAA	47	10	0.0003	1363
EVVEVVPISH	165	10	0.0002	1364
EVVPISHLY	168	9	0.0002	1365
FFPVIFSK	146	8		1366
FFPVIFSKA	146	9	0.0003	1367
FLLLKYRA	119	8		1368
FLLLKYRAR	119	9		1369
FSTTINYTLWR	71	11	0.0110	1370
GASSFSTTINY	67	11		1371
GDCAPEEK	213	8		1372
GDNQVMPK	191	8		1373
GGEPHISY	294	8		1374
GLEARGEA	15	8		1375
GLLGDNQVMPK	188	11	0.0780	1376
GLLIIVLA	200	8		1377
GLLIIVLAIIA	200	11		1378
GLVGAQAPA	24	9	0.0003	1379
GSDPACYEF	263	9		1380
GSSNQEEEGPR	86	11	-0.0002	1381
HCKPEEGLEA	9	10	0.0003	1382
HCKPEEGLEAR	9	11		1383
HFLLLKYR	118	8		1384
HFLLLKYRA	118	9	0.0016	1385
HFLLLKYRAR	118	10	0.0014	1386
HISYPPLH	298	8		1387
HISYPPLHER	298	10	0.0074	1388
HISYPPLHERA	298	11		1389
HSPQGASSF	63	9	0.0002	1390
HTLKIGGEPH	289	10		1391
IAIEGDCA	209	8		1392
IFSKASEY	150	8		1393
IGGEPHISY	293	9		1394
IIAIEGDCA	208	9		1395
IIVLAIIA	203	8		1396
ILVTCLGLSY	177	10	0.0036	1397
ISRKMVELVH	109	10	0.0002	1398
ISRKMVELVHF	109	11		1399
ISYPPLHER	299	9	0.0340	1400
ISYPPLHERA	299	10		1401
KAEMLESVLR	132	10	0.0002	1402
KASEYLQLVF	153	10	0.0002	1403
KIGGEPHISY	292	10		1404
KMVELVHF	112	8		1405
KTGLLIIVLA	198	10		1406
KVLHHTLK	285	8	0.0053	1407

Table XVI A

Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
LAIIAIEGDCA	206	11		1408
LGDNQVMPK	190	9	0.0002	1409
LGLVGAQA	23	8		1410
LGLVGAQAPA	23	10	0.0003	1411
LIETSYVK	278	8	-0.0004	1412
LIETSYVKVLH	278	11		1413
LIIVLAIIA	202	9		1414
LLGDNQVMPK	189	10	0.0093	1415
LLIIVLAIIA	201	10		1416
LLLKYRAR	120	8	-0.0009	1417
LLMQDLVQENY	245	11		1418
LMQDLVQENY	246	10		1419
LSMLEVFEGR	225	10	-0.0004	1420
LVEVTLGEVPA	45	11		1421
LVGAQAPA	25	8		1422
LVHFLLLK	116	8	0.0290	1423
LVHFLLLKY	116	9	0.0430	1424
LVHFLLLKYR	116	10	0.0260	1425
LVHFLLLKYRA	116	11		1426
LVQENYLEY	250	9		1427
LVQENYLEYR	250	10	0.0027	1428
LVTCLGLSY	178	9		1429
MFPDLESEF	97	9	0.0002	1430
MFPDLESEFQA	97	11		1431
MLEVFEGR	227	8	-0.0009	1432
MVELVHFLLLK	113	11	0.0200	1433
NCQDFFPVIF	142	10	0.0002	1434
PAADSPSPPH	54	10		1435
PACYEFLWGPR	266	11	-0.0009	1436
PATEEQQTA	31	9		1437
PDLESEFQA	99	9	0.0003	1438
PDLESEFQAA	99	10	0.0003	1439
PGSDPACY	262	8		1440
PGSDPACYEF	262	10		1441
PLEQRSQH	2	8		1442
PLEQRSQHCK	2	10	0.0003	1443
PLHERALR	303	8	-0.0009	1444
PSPPHSPQGA	59	10		1445
PVIFSKASEY	148	10	0.0160	1446
QAPATEEQQTA	29	11		1447
QDFFPVIF	144	8		1448
QDFFPVIFSK	144	10	0.0002	1449
QDFFPVIFSKA	144	11		1450
QDLVQENY	248	8		1451
QDLVQENYLEY	248	11		1452
QVPGSDPA	260	8		1453

Table XVI A

Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
QVPGSDPACY	260	10		1454
RALIETSY	276	8		1455
RALIETSYVK	276	10	0.0200	1456
RAREPVTK	125	8	-0.0009	1457
RAREPVTKA	125	9		1458
RGEALGLVGA	19	10	0.0003	1459
RMFPDLESEF	96	10	0.0002	1460
SDPACYEF	264	8		1461
SFSTTINY	70	8		1462
SMLEVFEGR	226	9	0.0020	1463
SSFSTTINY	69	9		1464
SSNQEEEGPR	87	10	0.0002	1465
STTINYTLWR	72	10	0.0014	1466
SVFAHPRK	237	8	0.1410	1467
SVLRNCQDF	138	9	0.0002	1468
SVLRNCQDFF	138	10	0.0002	1469
TGLLIIVLA	199	9		1470
TINYTLWR	74	8	0.0140	1471
TLGEVPAA	49	8		1472
TLKIGGEPH	290	9		1473
TSYVKVLH	281	8		1474
TSYVKVLHH	281	9	0.5900	1475
TTINYTLWR	73	9	0.0890	1476
VFEGREDSVF	230	10		1477
VFEGREDSVFA	230	11		1478
VIFSKASEY	149	9	0.0810	1479
VLRNCQDF	139	8		1480
VLRNCQDFF	139	9	0.0002	1481
VTCLGLSY	179	8		1482
VTLGEVPA	48	8		1483
VTLGEVPAA	48	9	0.0003	1484
VVEVVPISH	166	9	0.0007	1485
VVEVVPISHLY	166	11		1486
VVPISHLY	169	8		1487
WGPRALIETSY	273	11		1488
YILVTCLGLSY	176	11		1489
YVKVLHHTLK	283	10	0.0033	1490

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
AALSRKVA	107	8		1491
ACYEFLWGPR	267	10	0.0032	1492
ACYEFLWGPRA	267	11		1493
AGLLIIVLA	199	9	0.0006	1494
AIIAREGDCA	207	10		1495
ALGLVGAQA	22	9	0.0003	1496
ALGLVGAQAPA	22	11		1497
ALSRKVAELVH	108	11		1498
ALVETSYVK	277	9	0.0270	1499
ASSLPTTMNY	68	10	0.0009	1500
ASSSLQLVF	154	9	0.0011	1501
ATCLGLSY	179	8		1502
ATEEQEAA	32	8		1503
DLESEFQA	100	8		1504
DLESEFQAA	100	9		1505
DSILGDPK	236	8	-0.0004	1506
DSILGDPKK	236	9	-0.0003	1507
EALGLVGA	21	8		1508
EALGLVGAQA	21	10	0.0003	1509
EDSILGDPK	235	9	0.0003	1510
EDSILGDPKK	235	10	0.0003	1511
EFLWGPRA	270	8		1512
EFQAALSR	104	8		1513
EFQAALSRK	104	9	0.0002	1514
EFQAALSRKVA	104	11		1515
EGDCAPEEK	212	9	0.0002	1516
EGLEARGEA	14	9	0.0003	1517
ELMEVDPIGH	165	10	0.0003	1518
ELSVLEVF	224	8		1519
ELSVLEVFEGR	224	11	-0.0009	1520
ELVHFLLLK	115	9	0.0045	1521
ELVHFLLLKY	115	10	0.0066	1522
ELVHFLLLKYR	115	11	0.0011	1523
ESEFQAALSR	102	10	0.0002	1524
ESEFQAALSRK	102	11	0.0002	1525
ETSYVKVLH	280	9		1526
ETSYVKVLHH	280	10		1527
EVDPIGHLY	168	9	0.0002	1528
EVDPIGHLYIF	168	11		1529
EVTLGEVPA	47	9	0.0003	1530
EVTLGEVPAA	47	10	0.0003	1531
FATCLGLSY	178	9	0.0003	1532
FFPVIFSK	146	8		1533
FFPVIFSKA	146	9	0.0003	1534
FLLLKYRA	119	8		1535
FLLLKYRAR	119	9		1536

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
FVQENYLEY	250	9		1537
FVQENYLEYR	250	10	0.0009	1538
GASSLPTTMNY	67	11		1539
GDCAPEEK	213	8		1540
GDNQIMPK	191	8		1541
GDNQIMPKA	191	9	0.0003	1542
GDPKKLLTQH	240	10	0.0003	1543
GDPKKLLTQHF	240	11		1544
GGPHISYPPLH	295	11		1545
GLEARGEA	15	8		1546
GLLGDNQIMPK	188	11	0.1300	1547
GLLIIVLA	200	8		1548
GLLIIVLAIIA	200	11		1549
GLVGAQAPA	24	9	0.0003	1550
GSDPACYEF	263	9		1551
GSVVGNWQY	137	9		1552
GSVVGNWQYF	137	10	0.0020	1553
GSVVGNWQYFF	137	11		1554
HCKPEEGLEA	9	10	0.0003	1555
HCKPEEGLEAR	9	11		1556
HFLLLKYR	118	8		1557
HFLLLKYRA	118	9	0.0016	1558
HFLLLKYRAR	118	10	0.0014	1559
HFVQENYLEY	249	10		1560
HFVQENYLEYR	249	11		1561
HISYPPLH	298	8		1562
HMVKISGGPH	289	10		1563
IAREGDCA	209	8		1564
IFATCLGLSY	177	10	0.0005	1565
IGHLYIFA	172	8		1566
IIAREGDCA	208	9		1567
IIVLAIIA	203	8		1568
IIVLAIIAR	203	9	0.0069	1569
ISGGPHISY	293	9	0.0003	1570
IVLAIIAR	204	8	0.0053	1571
KAGLLIIVLA	198	10		1572
KASSSLQLVF	153	10	0.0003	1573
KISGGPHISY	292	10		1574
KVAELVHF	112	8		1575
KVLHHMVK	285	8	0.0580	1576
LAIIAREGDCA	206	11		1577
LGDNQIMPK	190	9		1578
LGDNQIMPKA	190	10	0.0003	1579
LGDPKKLLTQH	239	11		1580
LGLVGAQA	23	8		1581
LGLVGAQAPA	23	10	0.0003	1582

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
LGSVVGNWQY	136	10	0.0003	1583
LGSVVGNWQYF	136	11		1584
LIIVLAIIA	202	9		1585
LIIVLAIIAR	202	10	0.0280	1586
LLGDNQIMPK	189	10	0.0200	1587
LLGDNQIMPKA	189	11		1588
LLIIVLAIIA	201	10		1589
LLIIVLAIIAR	201	11	0.0021	1590
LLLKYRAR	120	8	-0.0009	1591
LLTQHFVQENY	245	11		1592
LMEVDPIGH	166	9	0.0002	1593
LMEVDPIGHLY	166	11		1594
LSRKVAELVH	109	10	0.0002	1595
LSRKVAELVHF	109	11		1596
LSVLEVFEGR	225	10	-0.0006	1597
LTQHFVQENY	246	10	0.0003	1598
LVETSYVK	278	8	-0.0004	1599
LVETSYVKVLH	278	11		1600
LVEVTLGEVPA	45	11		1601
LVGAQAPA	25	8		1602
LVHFLLLK	116	8	0.0290	1603
LVHFLLLKY	116	9	0.0430	1604
LVHFLLLKYR	116	10	0.0260	1605
LVHFLLLKYRA	116	11		1606
MLGSVVGNWQY	135	11		1607
MVKISGGPH	290	9	0.0003	1608
PACYEFLWGPR	266	11	-0.0009	1609
PATEEQEA	31	8		1610
PATEEQEAA	31	9	0.0003	1611
PDLESEFQA	99	9	0.0003	1612
PDLESEFQAA	99	10	0.0003	1613
PDPPQSPQGA	59	10	0.0003	1614
PGSDPACY	262	8		1615
PGSDPACYEF	262	10		1616
PIGHLYIF	171	8		1617
PIGHLYIFA	171	9		1618
PLEQRSQH	2	8		1619
PLEQRSQHCK	2	10	0.0003	1620
PLHEWVLR	303	8	-0.0009	1621
PSTFPDLESEF	95	11		1622
QAALSRKVA	106	9		1623
QAPATEEQEA	29	10	0.0003	1624
QAPATEEQEAA	29	11		1625
QVPGSDPA	260	8		1626
QVPGSDPACY	260	10		1627
RALVETSY	276	8		1628

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
RALVETSYVK	276	10	0.0190	1629
RAREPVTK	125	8	-0.0009	1630
RAREPVTKA	125	9		1631
RGEALGLVGA	19	10	0.0003	1632
SDPACYEF	264	8		1633
SGGPHISY	294	8		1634
SILGDPKK	237	8	-0.0009	1635
SLPTTMNY	70	8		1636
SSLPTTMNY	69	9		1637
SSSLQLVF	155	8		1638
STFPDLESEF	96	10	0.0002	1639
SVLEVFEGR	226	9	0.0003	1640
SVVGNWQY	138	8		1641
SVVGNWQYF	138	9	0.0002	1642
SVVGNWQYFF	138	10	0.0085	1643
TFPDLESEF	97	9	0.0002	1644
TFPDLESEFQA	97	11		1645
TLGEVPAA	49	8		1646
TMNYPLWSQSY	74	11		1647
TSYVKVLH	281	8		1648
TSYVKVLHH	281	9	0.5900	1649
VAELVHFLLLK	113	11	-0.0002	1650
VDPIGHLY	169	8		1651
VDPIGHLYIF	169	10	0.0003	1652
VDPIGHLYIFA	169	11		1653
VGNWQYFF	140	8		1654
VLEVFEGR	227	8	0.0016	1655
VTLGEVPA	48	8		1656
VTLGEVPAA	48	9	0.0003	1657
VVGNWQYF	139	8		1658
VVGNWQYFF	139	9	0.0022	1659
WGPRALVETSY	273	11		1660
YFFPVIFSK	145	9	0.0020	1661
YFFPVIFSKA	145	10	0.0003	1662
YIFATCLGLSY	176	11		1663
YVKVLHHMVK	283	10	0.0020	1664

Table XVII A
Mage 2 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
AADSPSPPH	55	9	0.0009	1665
ACYEFLWGPR	267	10	0.0035	1666
ADSPSPPH	56	8		1667
AIEGDCAPEEK	210	11	0.0007	1668
AISRKMVELVH	108	11		1669
ALIETSYVK	277	9	0.1900	1670
ASSFSTTINY	68	10	0.0260	1671
DFFPVIFSK	145	9	0.0022	1672
DLVQENYLEY	249	10		1673
DLVQENYLEYR	249	11	0.0018	1674
DSVFAHPR	236	8	0.0005	1675
DSVFAHPRK	236	9	0.0025	1676
EDSVFAHPR	235	9		1677
EDSVFAHPRK	235	10		1678
EFQAAISR	104	8		1679
EFQAAISRK	104	9	0.0002	1680
EGDCAPEEK	212	9	0.0001	1681
EGREDSVFAH	232	10		1682
ELSMLEVFEGR	224	11	0.0008	1683
ELVHFLLLK	115	9	0.0011	1684
ELVHFLLLKY	115	10	0.0003	1685
ELVHFLLLKYR	115	11	0.0031	1686
EMLESVLR	134	8	-0.0003	1687
ESEFQAAISR	102	10	0.0002	1688
ESEFQAAISRK	102	11	0.0004	1689
ETSYVKVLH	280	9		1690
ETSYVKVLHH	280	10		1691
EVVEVVPISH	165	10	0.0002	1692
EVVPISHLY	168	9	0.0002	1693
FFPVIFSK	146	8		1694
FLLLKYRAR	119	9		1695
FSTTINYTLWR	71	11	0.0170	1696
GASSFSTTINY	67	11		1697
GDCAPEEK	213	8		1698
GDNQVMPK	191	8		1699
GGEPHISY	294	8		1700
GLLGDNQVMPK	188	11	0.0047	1701
GSSNQEEEGPR	86	11	-0.0002	1702
HCKPEEGLEAR	9	11		1703
HFLLLKYR	118	8		1704
HFLLLKYRAR	118	10	0.0002	1705
HISYPPLH	298	8		1706
HISYPPLHER	298	10	0.0018	1707
HTLKIGGEPH	289	10		1708
IFSKASEY	150	8		1709
IGGEPHISY	293	9		1710

Table XVII A
Mage 2 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
ILVTCLGLSY	177	10	0.0002	1711
ISRKMVELVH	109	10	0.0002	1712
ISYPPLHER	299	9	0.0280	1713
KAEMLESVLR	132	10	0.0009	1714
KIGGEPHISY	292	10		1715
KVLHHTLK	285	8	0.0100	1716
LGDNQVMPK	190	9	0.0061	1717
LIETSYVK	278	8	0.0027	1718
LIETSYVKVLH	278	11		1719
LLGDNQVMPK	189	10	0.0014	1720
LLLKYRAR	120	8	-0.0004	1721
LLMQDLVQENY	245	11		1722
LMQDLVQENY	246	10		1723
LSMLEVFEGR	225	10	0.0001	1724
LVHFLLLK	116	8	0.1500	1725
LVHFLLLKY	116	9	0.0100	1726
LVHFLLLKYR	116	10	0.0022	1727
LVQENYLEY	250	9		1728
LVQENYLEYR	250	10	0.0089	1729
LVTCLGLSY	178	9		1730
MLEVFEGR	227	8	-0.0004	1731
MVELVHFLLLK	113	11	0.0120	1732
PAADSPSPPH	54	10		1733
PACYEFLWGPR	266	11	-0.0002	1734
PGSDPACY	262	8		1735
PLEQRSQH	2	8		1736
PLEQRSQHCK	2	10	0.0002	1737
PLHERALR	303	8	-0.0004	1738
PVIFSKASEY	148	10	0.0033	1739
QDFFPVIFSK	144	10	0.0083	1740
QDLVQENY	248	8		1741
QDLVQENYLEY	248	11		1742
QVPGSDPACY	260	10		1743
RALIETSY	276	8		1744
RALIETSYVK	276	10	0.0750	1745
RAREPVTK	125	8	-0.0003	1746
SFSTTINY	70	8		1747
SMLEVFEGR	226	9	0.0220	1748
SNQEEEGPR	88	9	0.0001	1749
SSFSTTINY	69	9		1750
SSNQEEEGPR	87	10	0.0002	1751
STTINYTLWR	72	10	0.0910	1752
SVFAHPRK	237	8	0.0810	1753
TINYTLWR	74	8	0.0550	1754
TLKIGGEPH	290	9		1755
TSYVKVLH	281	8		1756

Table XVII A

Mage 2 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
TSYVKVLHH	281	9	0.0066	1757
TTINYTLWR	73	9	1.1000	1758
VIFSKASEY	149	9	0.0330	1759
VTCLGLSY	179	8		1760
VVEVVPISH	166	9	0.0100	1761
VVEVVPISHLY	166	11		1762
VVPISHLY	169	8		1763
WGPRALIETSY	273	11		1764
YILVTCLGLSY	176	11		1765
YVKVLHHTLK	283	10	0.0160	1766

Table XVII B

Mage 3 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
ACYEFLWGPR	267	10	0.0035	1767
ALSRKVAELVH	108	11		1768
ALVETSYVK	277	9	0.1700	1769
ASSLPTTMNY	68	10	0.0330	1770
ATCLGLSY	179	8		1771
DSILGDPK	236	8	-0.0003	1772
DSILGDPKK	236	9	-0.0002	1773
EDSILGDPK	235	9	0.0002	1774
EDSILGDPKK	235	10	0.0002	1775
EFQAALSR	104	8		1776
EFQAALSRK	104	9	0.0001	1777
EGDCAPEEK	212	9	0.0001	1778
ELMEVDPIGH	165	10	0.0002	1779
ELSVLEVFEGR	224	11	0.0023	1780
ELVHFLLLK	115	9	0.0011	1781
ELVHFLLLKY	115	10	0.0003	1782
ELVHFLLLKYR	115	11	0.0031	1783
ESEFQAALSR	102	10	0.0002	1784
ESEFQAALSRK	102	11	0.0004	1785
ETSYVKVLH	280	9		1786
ETSYVKVLHH	280	10		1787
EVDPIGHLY	168	9	0.0009	1788
FATCLGLSY	178	9	0.0004	1789
FFPVIFSK	146	8		1790
FLLLKYRAR	119	9		1791
FVQENYLEY	250	9		1792
FVQENYLEYR	250	10	0.0012	1793
GASSLPTTMNY	67	11		1794
GDCAPEEK	213	8		1795
GDNQIMPK	191	8		1796
GDPKKLLTQH	240	10	0.0002	1797
GGPHISYPPLH	295	11		1798
GLLGDNQIMPK	188	11	0.0570	1799
GSVVGNWQY	137	9		1800
HCKPEEGLEAR	9	11		1801
HFLLLKYR	118	8		1802
HFLLLKYRAR	118	10	0.0002	1803
HFVQENYLEY	249	10		1804
HFVQENYLEYR	249	11		1805
HISYPPLH	298	8		1806
HMVKISGGPH	289	10		1807
IFATCLGLSY	177	10	0.0004	1808
IIVLAIIAR	203	9	0.0011	1809
ISGGPHISY	293	9	0.0002	1810
IVLAIIAR	204	8	0.0037	1811
KISGGPHISY	292	10		1812
KVLHHMVK	285	8	0.0190	1813

Table XVII B

Mage 3 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
LGDNQIMPK	190	9		1814
LGDPKKLLTQH	239	11		1815
LGSVVGNWQY	136	10	0.0012	1816
LIIVLAIIAR	202	10	0.0021	1817
LLGDNQIMPK	189	10	0.0110	1818
LLIIVLAIIAR	201	11	0.0056	1819
LLLKYRAR	120	8	-0.0004	1820
LLTQHFVQENY	245	11		1821
LMEVDPIGH	166	9	0.0001	1822
LMEVDPIGHLY	166	11		1823
LSRKVAELVH	109	10	0.0002	1824
LSVLEVFEGR	225	10	0.0030	1825
LTQHFVQENY	246	10	0.0002	1826
LVETSYVK	278	8	0.0014	1827
LVETSYVKVLH	278	11		1828
LVHFLLLK	116	8	0.1500	1829
LVHFLLLKY	116	9	0.0100	1830
LVHFLLLKYR	116	10	0.0022	1831
MLGSVVGNWQY	135	11		1832
MNYPLWSQSY	75	10	0.0002	1833
MVKISGGPH	290	9	0.0002	1834
PACYEFLWGPR	266	11	-0.0002	1835
PGSDPACY	262	8		1836
PLEQRSQH	2	8		1837
PLEQRSQHCK	2	10	0.0002	1838
PLHEWVLR	303	8	-0.0003	1839
QVPGSDPACY	260	10		1840
RALVETSY	276	8		1841
RALVETSYVK	276	10	0.1100	1842
RAREPVTK	125	8	-0.0003	1843
SGGPHISY	294	8		1844
SILGDPKK	237	8	0.0012	1845
SLPTTMNY	70	8		1846
SSLPTTMNY	69	9		1847
SVLEVFEGR	226	9	0.1400	1848
SVVGNWQY	138	8		1849
TMNYPLWSQSY	74	11		1850
TSYVKVLH	281	8		1851
TSYVKVLHH	281	9	0.0066	1852
VAELVHFLLLK	113	11	0.0011	1853
VDPIGHLY	169	8		1854
VLEVFEGR	227	8	0.0005	1855
WGPRALVETSY	273	11		1856
YFFPVIFSK	145	9	0.0270	1857
YIFATCLGLSY	176	11		1858
YVKVLHHMVK	283	10	0.0061	1859

Table XVIII A

Mage 2 A24 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
CYEFLWGPRAL	268	11	0.0004	1860
EFLWGPRAL	270	9	0.0006	1861
EFLWGPRALI	270	10	0.0097	1862
EYLQLVFGI	156	9	3.5000	1863
IFSKASEYL	150	9	0.0230	1864
IFSKASEYLQL	150	11	0.0950	1865
IWEELSML	221	8	0.0007	1866
IWEELSMLEVF	221	11	0.0170	1867
KMVELVHF	112	8	0.0005	1868
KMVELVHFL	112	9		1869
KMVELVHFLL	112	10		1870
KMVELVHFLLL	112	11		1871
LMQDLVQENYL	246	11		1872
LWGPRALI	272	8	0.1200	1873
LYILVTCL	175	8	0.0086	1874
LYILVTCLGL	175	10	0.0140	1875
MFPDLESEF	97	9	0.0140	1876
RMFPDLESEF	96	10	0.0016	1877
SFSTTINYTL	70	10	0.0150	1878
SFSTTINYTLW	70	11	0.0280	1879
SYPPLHERAL	300	10	0.0003	1880
SYVKVLHHTL	282	10	0.1600	1881
VFAHPRKL	238	8	0.0005	1882
VFAHPRKLL	238	9	0.0006	1883
VFEGREDSVF	230	10	0.0004	1884
VMPKTGLL	195	8	-0.0004	1885
VMPKTGLLI	195	9	0.2300	1886
VMPKTGLLII	195	10	0.0580	1887

Table XVIII B
Mage 3 A24 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
CYEFLWGPRAL	268	11	0.0004	1888
EFLWGPRAL	270	9	0.0006	1889
EMLGSVVGNW	134	10	0.0017	1890
HFVQENYL	249	8	-0.0004	1891
HMVKISGGPHI	289	11		1892
IFATCLGL	177	8	0.0120	1893
IFSKASSSL	150	9	0.0160	1894
IFSKASSSLQL	150	11	0.0910	1895
IMPKAGLL	195	8		1896
IMPKAGLLI	195	9	0.4200	1897
IMPKAGLLII	195	10	0.0500	1898
IWEELSVL	221	8	-0.0004	1899
IWEELSVLEVF	221	11	0.0260	1900
LMEVDPIGHL	166	10		1901
LYIFATCL	175	8	0.0140	1902
LYIFATCLGL	175	10	0.0480	1903
NWQYFFPVI	142	9	0.5300	1904
NWQYFFPVIF	142	10	0.0170	1905
QYFFPVIF	144	8	0.1200	1906
SYDGLLGDNQI	185	11	0.0026	1907
SYPPLHEW	300	8	0.0420	1908
SYPPLHEWVL	300	10	0.5900	1909
TFPDLESEF	97	9	0.0049	1910
VFEGREDSI	230	9	-0.0004	1911
VFEGREDSIL	230	10	-0.0005	1912

Table XIX A 1 Mage 2 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wβ1	DR2wβ2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LVGAQAPAT	2044	ALGLVGAQAPATEEQ	1913	24	0.0330				-0.0032			
LSYDGLLGD	2045	CLGLSYDGLLGDNQV	1914	183				0.1400				
LGDNQVMPK	2046	DGLLGDNQVMPKTGL	1915	189	-0.0005				-0.0032			
IWEELSMLE	2047	EEKIWEELSMLEVFE	1916	220				0.0130				
WGPRALIET	2048	EFLWGPRALIETSYV	1917	272								
WEELSMLEV	2049	EKIWEELSMLEVFEG	1918	221								
LEYRQVPGS	2050	ENYLEYRQVPGSDPA	1919	255								
ISYPPLHER	2051	EPHISYPPLHERALR	1920	298	-0.0003				-0.0032			
FQAAISRKM	2052	ESEFQAAISRKMVEL	1921	104	1.2000	0.0620	1.0000	0.0113	0.1600		0.0270	
LGEVPAADS	2053	EVTLGEVPAADSPSP	1922	49								
VIFSKASEY	2054	FFPVIFSKASEYLQL	1923	148								
IFSKASEYL	2055	FPVIFSKASEYLQLV	1924	149								
LGLVGAQAP	2056	GEALGLVGAQAPATE	1925	22								
VVEVVPISH	2057	GIEVVEVVPISHLYI	1926	165	0.0084	0.0046	0.0009	0.0036	0.0070		-0.0005	
IIVLAIIAI	2058	GLLIIVLAIIAIEGD	1927	202	0.0100				-0.0032			
LLKYRAREP	2059	HFLLLKYRAREPVTK	1928	120								
ILVTCLGLS	2060	HLYILVTCLGLSYDG	1929	176								
VEVVPISHL	2061	IEVVEVVPISHLYIL	1930	166								
IEGDCAPEE	2062	IIAIEGDCAPEEKIW	1931	210				0.0660				
LAIIAIEGD	2063	IIVLAIIAIEGDCAP	1932	205								
LYILVTCLG	2064	ISHLYILVTCLGLSY	1933	174								
MLESVLRNC	2065	KAEMLESVLRNCQDF	1934	134								
LLIIVLAII	2066	KTGLLIIVLAIIAIE	1935	200	0.0120	0.0037	-0.0022	0.0025	0.0370		-0.0005	
VPAADSPSP	2067	LGEVPAADSPSPPHS	1936	52	-0.0005				-0.0032			
VGAQAPATE	2068	LGLVGAQAPATEEQQ	1937	25								
VLAIIAIEG	2069	LIIVLAIIAIEGDCA	1938	204	0.0120				0.0051			
IVLAIIAIE	2070	LLIIVLAIIAIEGDC	1939	203	0.0086				0.0120			
YRAREPVTK	2071	LLKYRAREPVTKAEM	1940	123								
VFGIEVVEV	2072	LQLVFGIEVVEVVPI	1941	160								
VTLGEVPAA	2073	LVEVTLGEVPAADSP	1942	47								
LVHFLLLKY	2074	MVELVHFLLLKYRAR	1943	115								
MPKTGLLII	2075	NQVMPKTGLLIIVLA	1944	195	0.0019				-0.0032			
LLMQDLVQE	2076	PRKLLMQDLVQENYL	1945	244								
FPDLESEFQ	2077	PRMFPDLESEFQAAI	1946	97								
ISRKMVELV	2078	QAAISRKMVELVHFL	1947	108								
FPVIFSKAS	2079	QDFFPVIFSKASEYL	1948	146								
VQENYLEYR	2080	QDLVQENYLEYRQVP	1949	250								
FGIEVVEVV	2081	QLVFGIEVVEVVPIS	1950	161				0.0072				
IETSYVKVL	2082	RALIETSYVKVLHHT	1951	278								
VTKAEMLES	2083	REPVTKAEMLESVLR	1952	129								
LMQDLVQEN	2084	RKLLMQDLVQENYLE	1953	245				0.1500				
YILVTCLGL	2085	SHLYILVTCLGLSYD	1954	175								
LVEVTLGEV	2086	SSTLVEVTLGEVPAA	1955	44								
LIIVLAIIA	2087	TGLLIIVLAIIAIEG	1956	201	0.0008				-0.0032			
VHFLLLKYR	2088	VELVHFLLLKYRARE	1957	116								
VPISHLYIL	2089	VEVVPISHLYILVTC	1958	169								
IEVVEVVPI	2090	VFGIEVVEVVPISHL	1959	163								
ISHLYILVT	2091	VVPISHLYILVTCLG	1960	171								
LSMLEVFEG	2092	WEELSMLEVFEGRED	1961	224								
LWGPRALIE	2093	YEFLWGPRALIETSY	1962	271								
VTCLGLSYD	2094	YILVTCLGLSYDGLL	1963	178								
LHERALREG	2095	YPPLHERALREGEE-	1964	303								

Table XIX A 2 **Mage 2 DR Super Motif Peptides with Binding Data**

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LVGAQAPAT	2044	ALGLVGAQAPATEEQ	1913		-0.0011			
LSYDGLLGD	2045	CLGLSYDGLLGDNQV	1914					
LGDNQVMPK	2046	DGLLGDNQVMPKTGL	1915		-0.0011			
IWEELSMLE	2047	EEKIWEELSMLEVFE	1916					
WGPRALIET	2048	EFLWGPRALIETSYV	1917					
WEELSMLEV	2049	EKIWEELSMLEVFEG	1918					
LEYRQVPGS	2050	ENYLEYRQVPGSDPA	1919					
ISYPPLHER	2051	EPHISYPPLHERALR	1920		-0.0011			
FQAAISRKM	2052	ESEFQAAISRKMVEL	1921	0.0067	0.5100	0.0310		
LGEVPAADS	2053	EVTLGEVPAADSPSP	1922					
VIFSKASEY	2054	FFPVIFSKASEYLQL	1923					
IFSKASEYL	2055	FPVIFSKASEYLQLV	1924					
LGLVGAQAP	2056	GEALGLVGAQAPATE	1925					
VVEVVPISH	2057	GIEVVEVVPISHLYI	1926	0.0710	0.0900	0.0089		
IIVLAIIAI	2058	GLLIIVLAIIAIEGD	1927		-0.0011			
LLKYRAREP	2059	HFLLLKYRAREPVTK	1928					
ILVTCLGLS	2060	HLYILVTCLGLSYDG	1929					
VEVVPISHL	2061	IEVVEVVPISHLYIL	1930					
IEGDCAPEE	2062	IIAIEGDCAPEEKIW	1931					
LAIIAIEGD	2063	IIVLAIIAIEGDCAP	1932					
LYILVTCLG	2064	ISHLYILVTCLGLSY	1933					
MLESVLRNC	2065	KAEMLESVLRNCQDF	1934					
LLIIVLAII	2066	KTGLLIIVLAIIAIE	1935	0.0015	0.0290	-0.0004		
VPAADSPSP	2067	LGEVPAADSPSPPHS	1936		-0.0011			
VGAQAPATE	2068	LGLVGAQAPATEEQQ	1937					
VLAIIAIEG	2069	LIIVLAIIAIEGDCA	1938		0.0120			
IVLAIIAIE	2070	LLIIVLAIIAIEGDC	1939		0.0130			
YRAREPVTK	2071	LLKYRAREPVTKAEM	1940					
VFGIEVVEV	2072	LQLVFGIEVVEVVPI	1941					
VTLGEVPAA	2073	LVEVTLGEVPAADSP	1942					
LVHFLLLKY	2074	MVELVHFLLLKYRAR	1943					
MPKTGLLII	2075	NQVMPKTGLLIIVLA	1944		-0.0011			
LLMQDLVQE	2076	PRKLLMQDLVQENYL	1945					
FPDLESEFQ	2077	PRMFPDLESEFQAAI	1946					
ISRKMVELV	2078	QAAISRKMVELVHFL	1947					
FPVIFSKAS	2079	QDFFPVIFSKASEYL	1948					
VQENYLEYR	2080	QDLVQENYLEYRQVP	1949					
FGIEVVEVV	2081	QLVFGIEVVEVVPIS	1950					
IETSYVKVL	2082	RALIETSYVKVLHHT	1951					
VTKAEMLES	2083	REPVTKAEMLESVLR	1952					
LMQDLVQEN	2084	RKLLMQDLVQENYLE	1953					
YILVTCLGL	2085	SHLYILVTCLGLSYD	1954					
LVEVTLGEV	2086	SSTLVEVTLGEVPAA	1955					
LIIVLAIIA	2087	TGLLIIVLAIIAIEG	1956		-0.0011			
VHFLLLKYR	2088	VELVHFLLLKYRARE	1957					
VPISHLYIL	2089	VEVVPISHLYILVTC	1958					
IEVVEVVPI	2090	VFGIEVVEVVPISHL	1959					
ISHLYILVT	2091	VVPISHLYILVTCLG	1960					
LSMLEVFEG	2092	WEELSMLEVFEGRED	1961					
LWGPRALIE	2093	YEFLWGPRALIETSY	1962					
VTCLGLSYD	2094	YILVTCLGLSYDGLL	1963					
LHERALREG	2095	YPPLHERALREGEE-	1964					

Table XIX A 1 Mage 2 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VPGSDPACY	2096	YRQVPGSDPACYEFL	1965	260								
VLHHTLKIG	2097	YVKVLHHTLKIGGEP	1966	285								

Table XIX A 2 Mage 2 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VPGSDPACY	2096	YRQVPGSDPACYEFL	1965					
VLHHTLKIG	2097	YVKVLHHTLKIGGEP	1966					

Table XIX B 1 Mage 3 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VHFLLLKYR	2098	AELVHFLLLKYRARE	1967	116								
LIIVLAIIA	2099	AGLLIIVLAIIAREG	1968	201	0.0045				-0.0008			
LVGAQAPAT	2100	ALGLVGAQAPATEEQ	1969	24	0.0330				-0.0032			
LSYDGLLGD	2101	CLGLSYDGLLGDNQI	1970	183				-0.0025				
LGDNQIMPK	2102	DGLLGDNQIMPKAGL	1971	189	-0.0003				-0.0032			
IWEELSVLE	2103	EEKIWEELSVLEVFE	1972	220				0.0058				
WGPRALVET	2104	EFLWGPRALVETSYV	1973	272								
WEELSVLEV	2105	EKIWEELSVLEVFEG	1974	221								
LEYRQVPGS	2106	ENYLEYRQVPGSDPA	1975	255								
FQAALSRKV	2107	ESEFQAALSRKVAEL	1976	104	1.9000	0.3100	1.1000	0.0059	0.0590		0.0310	
LGEVPAAES	2108	EVTLGEVPAAESPDP	1977	49								
VIFSKASSS	2109	FFPVIFSKASSSLQL	1978	148								
IFSKASSSL	2110	FPVIFSKASSSLQLV	1979	149								
LGLVGAQAP	2111	GEALGLVGAQAPATE	1980	22								
YIFATCLGL	2112	GHLYIFATCLGLSYD	1981	175	0.0110				0.0110			
LMEVDPIGH	2113	GIELMEVDPIGHLYI	1982	165								
IIVLAIIAR	2114	GLLIIVLAIIAREGD	1983	202								
ISYPPLHEW	2115	GPHISYPPLHEWVLR	1984	298	0.0022				-0.0027			
LLKYRAREP	2116	HFLLLKYRAREPVTK	1985	120								
IFATCLGLS	2117	HLYIFATCLGLSYDG	1986	176								
MEVDPIGHL	2118	IELMEVDPIGHLYIF	1987	166	0.0003	0.0057	-0.0010	1.8000	-0.0055		-0.0008	
LYIFATCLG	2119	IGHLYIFATCLGLSY	1988	174								
MLGSVVGNW	2120	KAEMLGSVVGNWQYF	1989	134								
LLIIVLAII	2121	KAGLLIIVLAIIARE	1990	200	0.0043				-0.0008			
LTQHFVQEN	2122	KKLLTQHFVQENYLE	1991	245								
VPAAESPDP	2123	LGEVPAAESPDPPQS	1992	52								
VGAQAPATE	2124	LGLVGAQAPATEEQE	1993	25								
VLAIIAREG	2125	LIIVLAIIAREGDCA	1994	204								
IVLAIIARE	2126	LLIIVLAIIAREGDC	1995	203	0.0026				-0.0008			
YRAREPVTK	2127	LLKYRAREPVTKAEM	1996	123								
VFGIELMEV	2128	LQLVFGIELMEVDPI	1997	160	0.0250	0.0020	0.0013	0.0021	-0.0032		-0.0005	
VTLGEVPAA	2129	LVEVTLGEVPAAESP	1998	47								
MPKAGLLII	2130	NQIMPKAGLLIIVLA	1999	195	0.0440				-0.0032			
YFFPVIFSK	2131	NWQYFFPVIFSKASS	2000	144	0.1100	0.0030	0.0300	0.0006	0.1100		0.0650	
FPDLESEFQ	2132	PSTFPDLESEFQAAL	2001	97								
FSKASSSLQ	2133	PVIFSKASSSLQLVF	2002	150	0.0510	0.0170	-0.0007	0.0006	0.0240		-0.0005	
LSRKVAELV	2134	QAALSRKVAELVHFL	2003	108								
VQENYLEYR	2135	QHFVQENYLEYRQVP	2004	250								
FGIELMEVD	2136	QLVFGIELMEVDPIG	2005	161				0.0150				
FPVIFSKAS	2137	QYFFPVIFSKASSSL	2006	146								
VETSYVKVL	2138	RALVETSYVKVLHHM	2007	278								
VTKAEMLGS	2139	REPVTKAEMLGSVVG	2008	129								
LVEVTLGEV	2140	SSTLVEVTLGEVPAA	2009	44								
LVHFLLLKY	2141	VAELVHFLLLKYRAR	2010	115								
IGHLYIFAT	2142	VDPIGHLYIFATCLG	2011	171								
IELMEVDPI	2143	VFGIELMEVDPIGHL	2012	163								
WQYFFPVIF	2144	VGNWQYFFPVIFSKA	2013	142								
LSVLEVFEG	2145	WEELSVLEVFEGRED	2014	224								
LWGPRALVE	2146	YEFLWGPRALVETSY	2015	271								
LHEWVLREG	2147	YPPLHEWVLREGEE-	2016	303								
VPGSDPACY	2148	YRQVPGSDPACYEFL	2017	260								
VLHHMVKIS	2149	YVKVLHHMVKISGGP	2018	285								

Table XIX B 2 Mage 3 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VHFLLLKYR	2098	AELVHFLLLKYRARE	1967					
LIIVLAIIA	2099	AGLLIIVLAIIAREG	1968		-0.0026			
LVGAQAPAT	2100	ALGLVGAQAPATEEQ	1969		-0.0011			
LSYDGLLGD	2101	CLGLSYDGLLGDNQI	1970					
LGDNQIMPK	2102	DGLLGDNQIMPKAGL	1971		-0.0011			
IWEELSVLE	2103	EEKIWEELSVLEVFE	1972					
WGPRALVET	2104	EFLWGPRALVETSYV	1973					
WEELSVLEV	2105	EKIWEELSVLEVFEG	1974					
LEYRQVPGS	2106	ENYLEYRQVPGSDPA	1975					
FQAALSRKV	2107	ESEFQAALSRKVAEL	1976	0.0005	0.7400	0.0430		
LGEVPAAES	2108	EVTLGEVPAAESPDP	1977					
VIFSKASSS	2109	FFPVIFSKASSSLQL	1978					
IFSKASSSL	2110	FPVIFSKASSSLQLV	1979					
LGLVGAQAP	2111	GEALGLVGAQAPATE	1980					
YIFATCLGL	2112	GHLYIFATCLGLSYD	1981		0.0025			
LMEVDPIGH	2113	GIELMEVDPIGHLYI	1982					
IIVLAIIAR	2114	GLLIIVLAIIAREGD	1983					
ISYPPLHEW	2115	GPHISYPPLHEWVLR	1984		-0.0018			
LLKYRAREP	2116	HFLLLKYRAREPVTK	1985					
IFATCLGLS	2117	HLYIFATCLGLSYDG	1986					
MEVDPIGHL	2118	IELMEVDPIGHLYIF	1987	0.0130	0.0027	0.0130		
LYIFATCLG	2119	IGHLYIFATCLGLSY	1988					
MLGSVVGNW	2120	KAEMLGSVVGNWQYF	1989					
LLIIVLAII	2121	KAGLLIIVLAIIARE	1990		-0.0011			
LTQHFVQEN	2122	KKLLTQHFVQENYLE	1991					
VPAAESPDP	2123	LGEVPAAESPDPPQS	1992					
VGAQAPATE	2124	LGLVGAQAPATEEQE	1993					
VLAIIAREG	2125	LIIVLAIIAREGDCA	1994					
IVLAIIARE	2126	LLIIVLAIIAREGDC	1995		-0.0018			
YRAREPVTK	2127	LLKYRAREPVTKAEM	1996					
VFGIELMEV	2128	LQLVFGIELMEVDPI	1997	0.0004	0.0970	-0.0004		
VTLGEVPAA	2129	LVEVTLGEVPAAESP	1998					
MPKAGLLII	2130	NQIMPKAGLLIIVLA	1999		-0.0011			
YFFPVIFSK	2131	NWQYFFPVIFSKASS	2000	-0.0003	0.0560	0.2200		
FPDLESEFQ	2132	PSTFPDLESEFQAAL	2001					
FSKASSSLQ	2133	PVIFSKASSSLQLVF	2002	0.0240	0.0890	0.0038		
LSRKVAELV	2134	QAALSRKVAELVHFL	2003					
VQENYLEYR	2135	QHFVQENYLEYRQVP	2004					
FGIELMEVD	2136	QLVFGIELMEVDPIG	2005					
FPVIFSKAS	2137	QYFFPVIFSKASSSL	2006					
VETSYVKVL	2138	RALVETSYVKVLHHM	2007					
VTKAEMLGS	2139	REPVTKAEMLGSVVG	2008					
LVEVTLGEV	2140	SSTLVEVTLGEVPAA	2009					
LVHFLLLKY	2141	VAELVHFLLLKYRAR	2010					
IGHLYIFAT	2142	VDPIGHLYIFATCLG	2011					
IELMEVDPI	2143	VFGIELMEVDPIGHL	2012					
WQYFFPVIF	2144	VGNWQYFFPVIFSKA	2013					
LSVLEVFEG	2145	WEELSVLEVFEGRED	2014					
LWGPRALVE	2146	YEFLWGPRALVETSY	2015					
LHEWVLREG	2147	YPPLHEWVLREGEE-	2016					
VPGSDPACY	2148	YRQVPGSDPACYEFL	2017					
VLHHMVKIS	2149	YVKVLHHMVKISGGP	2018					

157
(deleted)

158
(deleted)

Table XXa A

Mage 2 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSYDGLLGD	2150	CLGLSYDGLLGDNQV	2019	183				0.1400				
IWEELSMLE	2151	EEKIWEELSMLEVFE	2020	220				0.0130				
LESEFQAAI	2152	FPDLESEFQAAISRK	2021	100				0.0033				
MFPDLESEF	2153	GPRMFPDLESEFQAA	2022	96				0.0890				
IEGDCAPEE	2154	IIAIEGDCAPEEKIW	2023	210				0.0660				
IAIEGDCAP	2155	LAIIAIEGDCAPEEK	2024	208				0.0190				
LVQENYLEY	2156	MQDLVQENYLEYRQV	2025	249				0.2000				
FGIEVVEVV	2157	QLVFGIEVVEVVPIS	2026	161				0.0072				
LMQDLVQEN	2158	RKLLMQDLVQENYLE	2027	245				0.1500				
LLGDNQVMP	2159	YDGLLGDNQVMPKTG	2028	188				0.0270				

Table XXa A

Mage 2 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSYDGLLGD	2150	CLGLSYDGLLGDNQV	2019					
IWEELSMLE	2151	EEKIWEELSMLEVFE	2020					
LESEFQAAI	2152	FPDLESEFQAAISRK	2021					
MFPDLESEF	2153	GPRMFPDLESEFQAA	2022					
IEGDCAPEE	2154	IIAIEGDCAPEEKIW	2023					
IAIEGDCAP	2155	LAIIAIEGDCAPEEK	2024					
LVQENYLEY	2156	MQDLVQENYLEYRQV	2025					
FGIEVVEVV	2157	QLVFGIEVVEVVPIS	2026					
LMQDLVQEN	2158	RKLLMQDLVQENYLE	2027					
LLGDNQVMP	2159	YDGLLGDNQVMPKTG	2028					

Table XXa B

Mage 3 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSYDGLLGD	2160	CLGLSYDGLLGDNQI	2029	183				-0.0025				
IWEELSVLE	2161	EEKIWEELSVLEVFE	2030	220				0.0058				
LESEFQAAL	2162	FPDLESEFQAALSRK	2031	100				0.0026				
MEVDPIGHL	2163	IELMEVDPIGHLYIF	2032	166	0.0003	0.0057	-0.0010	1.8000	-0.0055		-0.0008	
IAREGDCAP	2164	LAIIAREGDCAPEEK	2033	208				-0.0025				
FGIELMEVD	2165	QLVFGIELMEVDPIG	2034	161				0.0150				
FVQENYLEY	2166	TQHFVQENYLEYRQV	2035	249				0.2800				
LLGDNQIMP	2167	YDGLLGDNQIMPKAG	2036	188				0.0080				

Table XXa B

Mage 3 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSYDGLLGD	2160	CLGLSYDGLLGDNQI	2029					
IWEELSVLE	2161	EEKIWEELSVLEVFE	2030					
LESEFQAAL	2162	FPDLESEFQAALSRK	2031					
MEVDPIGHL	2163	IELMEVDPIGHLYIF	2032	0.0130	0.0027	0.0130		
IAREGDCAP	2164	LAIIAREGDCAPEEK	2033					
FGIELMEVD	2165	QLVFGIELMEVDPIG	2034					
FVQENYLEY	2166	TQHFVQENYLEYRQV	2035					
LLGDNQIMP	2167	YDGLLGDNQIMPKAG	2036					

Table XXb A

Mage 2 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
AAISRKMVE	2168	EFQAAISRKMVELVH	2037	106				0.0039				
MPLEQRSQH	2169	MPLEQRSQHCKP	2038	1								
IGGEPHISY	2170	TLKIGGEPHISYPPL	2039	292				-0.0025				
LHHTLKIGG	2171	VKVLHHTLKIGGEPH	2040	286				-0.0025				

Table XXb A

Mage 2 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
AAISRKMVE	2168	EFQAAISRKMVELVH	2037					
MPLEQRSQH	2169	MPLEQRSQHCKP	2038					
IGGEPHISY	2170	TLKIGGEPHISYPPL	2039					
LHHTLKIGG	2171	VKVLHHTLKIGGEPH	2040					

Table XXb B

Mage 3 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
ILGDPKKLL	2172	EDSILGDPKKLLTQH	2041	237	0.0003	-0.0006	-0.0010	0.6700	-0.0055		-0.0008	
AALSRKVAE	2173	EFQAALSRKVAELVH	2042	106				0.0027				
MPLEQRSQH	2174	MPLEQRSQHCKP	2043	1								

Table XXb B

Mage 3 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
ILGDPKKLL	2172	EDSILGDPKKLLTQH	2041	0.0130	-0.0014	0.0029		
AALSRKVAE	2173	EFQAALSRKVAELVH	2042					
MPLEQRSQH	2174	MPLEQRSQHCKP	2043					

Table XXII. A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
MAGE3.112	9	KVAELVHFL	2214	69	29	14	168	17	5
MAGE3.112L2	9	KLAELVHFL	2215	20	6.0	5.9	12	400	5
MAGE3.112M2	9	KMAELVHFL	2216	24	6.7	7.7	26	286	5
MAGE3.112L2V9	9	KLAELVHFV	2217	14	13	22	15	73	5
MAGE3.112M2V9	9	KMAELVHFV	2218	26	17	46	39	170	5
MAGE3.220	9	KIWEELSVL	2219	333	391	2381	308	--	3
MAGE3.220L2V9	9	KLWEELSVV	2220	11	165	20	15	--	4

-- indicates binding affinity =10,000nM.

Table XXIIA A01 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0101 nM
52.0026	8	ATCLGLSY	2221	MAGE3.179	227.3
52.013	11	VVEVVPISHLY	2222	MAGE2.166	125
52.0132	11	TMNYPLWSQSY	2223	MAGE3.74	301.2
52.0133	11	LMEVDPIGHLY	2224	MAGE3.166	3.3
57.0003	8	VTDLGLSY	2225	MAGE2.179.D3	2.7
57.0029	9	STFSTTINY	2226	MAGE2.69.T2	490.2
57.003	9	MTDLVQENY	2227	MAGE2.247.T2	0.8
57.0031	9	STLPTTMNY	2228	MAGE3.69.T2	58.1
57.0032	9	GTVVGNWQY	2229	MAGE3.137.T2	36.2
57.0033	9	ETDPIGHLY	2230	MAGE3.168.T2	0.7
57.0034	9	ITGGPHISY	2231	MAGE3.293.T2	36.2
57.0119	10	ATSFSTTINY	2232	MAGE2.68.T2	454.5
57.012	10	ASDFSTTINY	2233	MAGE2.68.D3	25
57.0121	10	LTQDLVQENY	2234	MAGE2.246.T2	58.1
57.0122	10	ATSLPTTMNY	2235	MAGE3.68.T2	208.3
57.0123	10	ASDLPTTMNY	2236	MAGE3.68.D3	2.6
57.0124	10	LTDHFVQENY	2237	MAGE3.246.D3	2.3

Table XXIIB A03 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.63	9	SVFSTTINK	2238	MAGE2.69.V2K9	20	8.2	3333.3	9666.7	5.7	3
1371.64	9	SVFSTTINR	2239	MAGE2.69.V2R9	57.9	6.3	62.1	87.9	6.7	5
1371.65	9	TVINYTLWR	2240	MAGE2.73.V2	261.9	76.9	720	432.8	14.5	4
1371.66	9	TVINYTLWK	2241	MAGE2.73.V2K9	305.6	96.8	9000	-58000	61.5	3
1371.68	9	LVHFLLLKR	2242	MAGE2/3.116.R9	440	375	236.8	93.5	26.7	5
1371.69	9	YVFPVIFSK	2243	MAGE3.138.V2	24.4	3	2769.2	783.8	1.7	3
1371.7	9	YVFPVIFSR	2244	MAGE3.138.V2R9	35.5	2.6	6	13.2	0.5	5
1371.71	8	SVFAHPRR	2245	MAGE2.237.R8	687.5	1538.5	620.7	580	156.9	1
1371.72	9	AVIETSYVK	2246	MAGE2.277.V2	392.9	62.5	12857.1	-290000	30.8	3
1371.73	9	AVIETSYVR	2247	MAGE2.277.V2R9	36666.7	171.4	128.6	1160	15.4	3
1371.74	9	IVYPPLHER	2248	MAGE2.299.V2	117	375	94.7	32.2	13.8	5
1371.75	9	IVYPPLHEK	2249	MAGE2.299.V2K9	42.3	103.4	857.1	2989.7	42.1	3

Table XXIIC A24 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*2401 nM
52.0072	8	LWGPRALI	2250	MAGE2.272	100
52.0073	8	QYFFPVIF	2251	MAGE3.144	100
52.0078	8	SYPPLHEW	2252	MAGE3.300	285.7
52.0102	10	SYPPLHEWVL	2253	MAGE3.300	20.3
52.0166	11	SFSTTINYTLW	2254	MAGE2.70	428.6
52.0167	11	IFSKASEYLQL	2255	MAGE2.150	126.3
52.017	11	IFSKASSSLQL	2256	MAGE3.150	131.9
52.0172	11	IWEELSVLEVF	2257	MAGE3.221	461.5
57.006	9	MYPDLESEF	2258	MAGE2.97.Y2	52.2
57.0061	9	KYVELVHFF	2259	MAGE2.112.Y2F9	7.1
57.0062	9	IYSKASEYF	2260	MAGE2.150.Y2F9	14.6
57.0063	9	EYLQLVFGF	2261	MAGE2.156.F9	4
57.0064	9	VYPKTGLLF	2262	MAGE2.195.Y2F9	5.5
57.0065	9	TYPDLESEF	2263	MAGE3.97.Y2	218.2
57.0066	9	NYQYFFPVF	2264	MAGE3.142.Y2F9	3.4
57.0067	9	IYSKASSSF	2265	MAGE3.150.Y2F9	375
57.0068	9	IYPKAGLLF	2266	MAGE3.195.Y2F9	9.2
57.0084	10	SYSTTINYTF	2267	MAGE2.70.Y2F10	14.8
57.0085	10	LYILVTCLGF	2268	MAGE2.175.F10	17.6
57.0086	10	VYPKTGLLIF	2269	MAGE2.195.Y2F10	2.9
57.0087	10	EYLWGPRALF	2270	MAGE2.270.Y2F10	10
57.0088	10	SYVKVLHHTF	2271	MAGE2.282.F10	34.3
57.009	10	NYQYFFPVIF	2272	MAGE3.142.Y2	22.6
57.0092	10	LYIFATCLGF	2273	MAGE3.175.F10	10
57.0093	10	IYPKAGLLIF	2274	MAGE3.195.Y2F10	1.2
57.0095	10	SYPPLHEWVF	2275	MAGE3.300.F10	5.5

Table XXIII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type [1]	CTL Tumor
MAGE2.112	9	KMVELVHFL	2276	9.8	25	17	123	2353	4	1/1	0/1
MAGE2.112	10	KMVELVHFLL	2277	23	39	127	9.0	2667	4	1/1	0/1
MAGE2.112	11	KMVELVHFLLL	2278	5.0	45	63	109	7692	4	1/1	0/1
MAGE2.153	9	KASEYLQLV	2279	152	116	17	185	4878	4	2/4	0/2
MAGE2.157	10	YLQLVFGIEV	2280	50	165	345	370	9302	4	3/3	1/3
MAGE2.160	10	LVFGIEVVEV	2281	357	20	43	28	8.0	5	4/4	0/3
MAGE3.112	9	KVAELVHFL	2282	68	29	14	168	17	5	3/4	3/4
MAGE3.112	10	KVAELVHFLL	2283	54	36	217	206	11	5	0/1	0/1
MAGE3.159	11	QLVFGIELMEV	2284	7.9	74	217	185	267	5	3/3	1/3[2]
MAGE3.160	10	LVFGIELMEV	2285	29	20	7.7	28	14	5	4/4	1/4[2]
MAGE3.195	11	IMPKAGLLIIV	2286	20	226	14	176	--[3]	4	3/4	0/3
MAGE3.220	9	KIWEELSVL	2287	357	391	2381	308	--	3	3/4	0/3
MAGE3.271	9	FLWGPRALV	2288	31	43	14	336	40	5	4/4	2/4

1) Indicates the number of donors positive over the total number of donors tested.

2) A positive result was seen after the second restim.

3) -- indicates binding affinity =10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		
				Source	Sequence	SEQ ID NO:
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	2289
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV	2290
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	2291
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	2292
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	2293
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	2294
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	2295
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	2296
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	2297
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	2298
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	2299
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVRR	2300
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	2301
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVYLL	2302
	B8	B*0801	Steinlin	HIVgp 586-593 Y1->F, Q5->Y	FLKDYQLL	2303
	B27	B*2705	LG2	R 60s	FRYNGLIHR	2304
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF	2305
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	2306
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	2307
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	2308
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	2309
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	2310
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	2311
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL	2312
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	2313
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	2314
Mouse	D^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	2315
	K^b		EL4	VSV NP 52-59	RGYVFQGL	2316
	D^d		P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	2317
	K^d		P815	non-natural (KdCON1)	KFNPMKTYI	2318
	L^d		P815	HBVs 28-39	IPQSLDSYWTSL	2319

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		
				Source	Sequence	SEQ ID NO:
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVKQNTLKLAT	2320
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY	2321
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAAAFA	2322
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR	2323
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	2324
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	2325
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	2326
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	2327
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE	2328
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE	2329
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE	2330
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE	2331
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE	2332
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS	2333
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE	2334
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE	2335
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVKQNTLKLAT	2336
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL	2337
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT	2338
	DQ3.1	)QA1*0301/DQB1*03(	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2339
Mouse	IA^b		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2340
	IA^d		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2341
	IA^k		CH-12	HEL 46-61	YNTDGSTDYGILQINSR	2342
	IA^s		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2343
	IA^u		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2344
	IE^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK	2345
	IE^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK	2346

Table XXVI. Crossbinding data A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
MAGE2.112	9	KMVELVHFL	2347	38	15	9.1	49	364	5
MAGE2.112	10	KMVELVHFLL	2348	23	39	127	9.0	2667	4
MAGE2.112	11	KMVELVHFLLL	2349	5.0	45	63	109	7692	4
MAGE2.153	9	KASEYLQLV	2350	152	116	17	185	4878	4
MAGE2.157	10	YLQLVFGIEV	2351	50	165	345	370	9302	4
MAGE2.160	10	LVFGIEVVEV	2352	357	21	44	29	8.0	5
MAGE2.220	9	KIWEELSML	2353	167	642	175	29	--	3
MAGE2.271	9	FLWGPRALI	2354	238	96	137	1542	95	4
MAGE2.277	10	ALIETSYVKV	2355	500	729	125	1947	3077	2
MAGE2/3.44	10	TLVEVTLGEV	2356	67	39	4.3	218	33	5
MAGE3.112	9	KVAELVHFL	2357	68	29	14	168	17	5
MAGE3.112	10	KVAELVHFLL	2358	54	36	217	206	11	5
MAGE3.159	11	QLVFGIELMEV	2359	7.9	74	217	185	267	5
MAGE3.160	10	LVFGIELMEV	2360	29	20	7.7	29	14	5
MAGE3.174	11	HLYIFATCLGL	2361	56	741	769	--	4494	1
MAGE3.176	9	YIFATCLGL	2362	185	45	37	1028	222	4
MAGE3.195	11	IMPKAGLLIIV	2363	20	226	15	176	--	4
MAGE3.220	9	KIWEELSVL	2364	333	391	2381	308	--	3
MAGE3.271	9	FLWGPRALV	2365	31	43	14	336	40	5

-- indicates binding affinity =10,000nM.

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type [1]	CTL Tumor
MAGE2.112	9	KMVELVHFL	2366	9.8	25	17	123	2353	4	1/1	0/1
MAGE2.112	10	KMVELVHFLL	2367	23	39	127	9.0	2667	4	1/1	0/1
MAGE2.112	11	KMVELVHFLLL	2368	5.0	45	63	109	7692	4	1/1	0/1
MAGE2.153	9	KASEYLQLV	2369	152	116	17	185	4878	4	2/4	0/2
MAGE2.157	10	YLQLVFGIEV	2370	50	165	345	370	9302	4	3/3	1/3
MAGE2.160	10	LVFGIEVVEV	2371	357	20	43	28	8.0	5	4/4	0/3
MAGE3.112	9	KVAELVHFL	2372	68	29	14	168	17	5	3/4	3/4
MAGE3.112	10	KVAELVHFLL	2373	54	36	217	206	11	5	0/1	0/1
MAGE3.159	11	QLVFGIELMEV	2374	7.9	74	217	185	267	5	3/3	1/3[2]
MAGE3.160	10	LVFGIELMEV	2375	29	20	7.7	28	14	5	4/4	1/4[2]
MAGE3.195	11	IMPKAGLLIIV	2376	20	226	14	176	-- [3]	4	3/4	0/3
MAGE3.220	9	KIWEELSVL	2377	357	391	2381	308	--	3	3/4	0/3
MAGE3.271	9	FLWGPRALV	2378	31	43	14	336	40	5	4/4	2/4

1) Indicates the number of donors positive over the total number of donors tested.
2) A positive result was seen after the second restim.
3) -- indicates binding affinity =10,000nM.

Table XXVIII. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross-binding
39.0282	2	LGEVPAADSPSPPHS	2379	MAGE2.50	--	--	--	0
39.0283	3	ESEFQAAISRKMVEL	2380	MAGE2.102	4.2	281	49	3
39.0284	2	GIEVVEVVPISHLYI	2381	MAGE2.163	595	6429	278	2
39.0285	2	DGLLGDNQVMPKTGL	2382	MAGE2.187	--	--	--	0
39.0286	2	NQVMPKTGLLIIVLA	2383	MAGE2.193	2632	--	--	0
39.0287	2	KTGLLIIVLAIIAIE	2384	MAGE2.198	417	1216	862	2
39.0288	2	TGLLIIVLAIIAIEG	2385	MAGE2.199	6250	--	--	0
39.0291	2	GLLIIVLAIIAIEGD	2386	MAGE2.200	500	--	--	1
39.0292	3	LLIIVLAIIAIEGDC	2387	MAGE2.201	581	3750	1923	1
39.0293	2	LIIVLAIIAIEGDCA	2388	MAGE2.202	417	8824	2083	1
39.0294	2	EPHISYPPLHERALR	2389	MAGE2.296	--	--	--	0
39.0295	3	ALGLVGAQAPATEEQ	2390	MAGE2/3.22	152	--	--	1
39.0296	2	ESEFQAALSRKVAEL	2391	MAGE3.102	2.6	763	34	3
39.0297	2	NWQYFFPVIFSKASS	2392	MAGE3.142	46	409	446	3
39.0298	3	PVIFSKASSSLQLVF	2393	MAGE3.148	98	1875	281	2
39.0299	3	LQLVFGIELMEVDPI	2394	MAGE3.158	200	--	258	2
39.0300	3	GHLYIFATCLGLSYD	2395	MAGE3.173	455	4091	--	1
39.0301	2	DGLLGDNQIMPKAGL	2396	MAGE3.187	--	--	--	0
39.0302	2	NQIMPKAGLLIIVLA	2397	MAGE3.193	114	--	--	1
39.0303	2	KAGLLIIVLAIIARE	2398	MAGE3.198	1163	--	--	0
39.0304	2	AGLLIIVLAIIAREG	2399	MAGE3.199	1111	--	>9615	0
39.0305	3	LLIIVLAIIAREGDC	2400	MAGE3.201	1923	--	--	0
39.0306	2	GPHISYPPLHEWVLR	2401	MAGE3.296	2273	--	--	0

-- indicates binding affinity =10,000nM.

Table XXIX. DR supertype crossbinding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 β1 nM	DR2w2 β2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR 147 Cross-binding	Broad Binding (5/8)
39.0283	ESEFQAAISRKMVEL	2402	MAGE2.102	4.2	281	49	147	20	522	741	1581	3	7
39.0284	GIEVVEVVPISHLYI	2403	MAGE2.163	595	6429	278	1978	--	49	--	5506	2	3
39.0287	KTGLLIIVLAIIAIE	2404	MAGE2.198	417	1216	862	2460	--	2333	--	--	2	2
39.0296	ESEFQAALSRKVAEL	2405	MAGE3.102	2.6	763	34	29	18	7000	645	1140	3	6
39.0297	NWQYFFPVIFSKASS	2406	MAGE3.142	46	409	446	3033	667	--	308	223	3	6
39.0298	PVIFSKASSSLQLVF	2407	MAGE3.148	98	1875	281	535	--	146	--	--	2	4
39.0299	LQLVFGIELMEVDPI	2408	MAGE3.158	200	--	258	4550	--	8750	--	--	2	2

-- indicates binding affinity =10,000nM.

Table XXX. DR3 binding

Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0384	GPRMFPDLESEFQAA	2409	MAGE2.94	3371
39.0387	FPDLESEFQAAISRK	2410	MAGE2.98	--
39.0388	EFQAAISRKMVELVH	2411	MAGE2.104	--
39.0389	QLVFGIEVVEVVPIS	2412	MAGE2.159	--
39.0390	CLGLSYDGLLGDNQV	2413	MAGE2.181	2143
39.0391	YDGLLGDNQVMPKTG	2414	MAGE2.186	--
39.0392	LAIIAIEGDCAPEEK	2415	MAGE2.206	--
39.0393	IIAIEGDCAPEEKIW	2416	MAGE2.208	4546
39.0394	EEKIWEELSMLEVFE	2417	MAGE2.218	--
39.0395	RKLLMQDLVQENYLE	2418	MAGE2.243	2000
39.0396	MQDLVQENYLEYRQV	2419	MAGE2.247	1500
39.0397	VKVLHHTLKIGGEPH	2420	MAGE2.284	--
39.0398	TLKIGGEPHISYPPL	2421	MAGE2.290	--
39.0399	FPDLESEFQAALSRK	2422	MAGE3.98	--
39.0400	EFQAALSRKVAELVH	2423	MAGE3.104	--
39.0401	QLVFGIELMEVDPIG	2424	MAGE3.159	--
39.0402	IELMEVDPIGHLYIF	2425	MAGE3.164	167
39.0403	CLGLSYDGLLGDNQI	2426	MAGE3.181	--
39.0404	YDGLLGDNQIMPKAG	2427	MAGE3.186	--
39.0405	LAIIAREGDCAPEEK	2428	MAGE3.206	--
39.0406	EEKIWEELSVLEVFE	2429	MAGE3.218	--
39.0407	EDSILGDPKKLLTQH	2430	MAGE3.235	448
39.0408	TQHFVQENYLEYRQV	2431	MAGE3.247	1071

-- indicates binding affinity =10,000nM.

Table XXXI. HTL Candidates

Peptide	Sequence	SEQ ID NO:	Motif	Source	DR1 nM	DR4w4 nM	DR7 nM	DR3 nM	DR2w2 β1 nM	DR2w2 β2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR 147 Cross-binding	Broad Binding (5/8)	DR3 Binder
39.0283	ESEFQAAISRKMVEL	2432	DR sup	MAGE2.102	4.2	281	49	--	147	20	522	741	1581	3	7	0
39.0296	ESEFQAALSRKVAEL	2433	DR sup	MAGE3.102	3	763	34	--	29	18	7000	645	1140	3	6	0
39.0297	NWQYFFPVIFSKASS	2434	DR sup	MAGE3.142	46	409	446	--	3033	667	--	308	223	3	6	0
39.0402	IELMEVDPIGHLYIF	2435	DR3	MAGE3.164	--	>8182	9259	167	1597	--	269	--	3769	0	1	1
39.0407	EDSILGDPKKLLTQH	2436	DR3	MAGE3.235	--	>8182	--	448	--	--	269	--	--	0	1	1

-- indicates binding affinity =10,000nM.

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	2175	25
A*0201	941.01	FLPSDYFPSV	2176	5.0
A*0202	941.01	FLPSDYFPSV	2177	4.3
A*0203	941.01	FLPSDYFPSV	2178	10
A*0205	941.01	FLPSDYFPSV	2179	4.3
A*0206	941.01	FLPSDYFPSV	2180	3.7
A*0207	941.01	FLPSDYFPSV	2181	23
A*6802	1072.34	YVIKVSARV	2182	8.0
A*0301	941.12	KVFPYALINK	2183	11
A*1101	940.06	AVDLYHFLK	2184	6.0
A*3101	941.12	KVFPYALINK	2185	18
A*3301	1083.02	STLPETYVVRR	2186	29
A*6801	941.12	KVFPYALINK	2187	8.0
A*2402	979.02	AYIDNYNKF	2188	12
B*0702	1075.23	APRTLVYLL	2189	5.5
B*3501	1021.05	FPFKYAAAF	2190	7.2
B51	1021.05	FPFKYAAAF	2191	5.5
B*5301	1021.05	FPFKYAAAF	2192	9.3
B*5401	1021.05	FPFKYAAAF	2193	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO: #	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	2194	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	2195	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	2196	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	2197	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	2198	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	2199	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	2200	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	2201	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	2202	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	2203	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	2204	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	2205	3.5
DRB1*1501	DR2w2β1	507.02	GRTQDENPVVHFFKNI VTPRTPPP	2206	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	2207	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	2208	58
DRB5*0101	DR2w2β2	553.01	QYIKANSKFIGITE	2209	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table VII A
Mage 2 A01 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASEYLQLVF	154	9		1
ASSFSTTINY	68	10	0.1700	2
DLVQENYLEY	249	10		3
ELSMLEVF	224	8		4
ELVHFLLLKY	115	10		5
ESVLRNCQDF	137	10		6
ESVLRNCQDFF	137	11		7
EVFEGREDSVF	229	11		8
EVVPISHLY	168	9	0.0028	9
FSTTINYTLW	71	10		10
GSDPACYEF	263	9		11
GSDPACYEFLW	263	11		12
HSPQGASSF	63	9		13
ILVTCLGLSY	177	10		14
ISRKMVELVHF	109	11		15
KIGGEPHISY	292	10		16
KMVELVHF	112	8		17
LLMQDLVQENY	245	11		18
LMQDLVQENY	246	10	0.0450	19
LVHFLLLKY	116	9		20
LVQENYLEY	250	9		21
LVTCLGLSY	178	9		22
PVIFSKASEY	148	10		23
QVPGSDPACY	260	10		24
RMFPDLESEF	96	10		25
SSFSTTINY	69	9	0.0430	26
STTINYTLW	72	9		27
SVLRNCQDF	138	9		28
SVLRNCQDFF	138	10		29
TTINYTLW	73	8		30
VIFSKASEY	149	9		31
VLRNCQDF	139	8		32
VLRNCQDFF	139	9		33
VTCLGLSY	179	8		34
VVEVVPISHLY	166	11	0.2000	35
VVPISHLY	169	8		36
YILVTCLGLSY	176	11		37

Table VII B

Mage 3 A01 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASSLPTTMNY	68	10	2.6000	38
ASSSLQLVF	154	9		39
ATCLGLSY	179	8	0.1100	40
ELSVLEVF	224	8		41
ELVHFLLLKY	115	10		42
EMLGSVVGNW	134	10		43
EVDPIGHLY	168	9	18.0000	44
EVDPIGHLYIF	168	11		45
FVQENYLEY	250	9		46
GSDPACYEF	263	9		47
GSDPACYEFLW	263	11		48
GSVVGNWQY	137	9	0.0500	49
GSVVGNWQYF	137	10		50
GSVVGNWQYFF	137	11		51
HISYPPLHEW	298	10		52
ISGGPHISY	293	9	0.0370	53
ISYPPLHEW	299	9		54
KISGGPHISY	292	10	0.0011	55
KVAELVHF	112	8		56
LLTQHFVQENY	245	11		57
LMEVDPIGHLY	166	11	7.5000	58
LSRKVAELVHF	109	11		59
LTQHFVQENY	246	10	0.2600	60
LVHFLLLKY	116	9		61
MLGSVVGNW	135	9		62
MLGSVVGNWQY	135	11		63
PIGHLYIF	171	8		64
PSTFPDLESEF	95	11		65
PTTMNYPLW	72	9		66
QVPGSDPACY	260	10		67
SLPTTMNY	70	8		68
SLPTTMNYPLW	70	11		69
SSLPTTMNY	69	9	0.0550	70
SSSLQLVF	155	8		71
STFPDLESEF	96	10		72
SVVGNWQY	138	8		73
SVVGNWQYF	138	9		74
SVVGNWQYFF	138	10		75
TMNYPLWSQSY	74	11	0.0830	76
TTMNYPLW	73	8		77
VVGNWQYF	139	8		78
VVGNWQYFF	139	9		79
YIFATCLGLSY	176	11		80

Table VIII A
Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
AAISRKMV	107	8						81
AAISRKMVEL	107	10						82
AAISRKMVELV	107	11						83
AIIAIEGDCA	207	10						84
AISRKMVEL	108	9						85
AISRKMVELV	108	10						86
ALGLVGAQA	22	9						87
ALGLVGAQAPA	22	11						88
ALIETSYV	277	8						89
ALIETSYVKV	277	10						90
ALIETSYVKVL	277	11						91
AQAPATEEQQT	28	11						92
ATEEQQTA	32	8						93
CAPEEKIWEEL	215	11						94
CLGLSYDGL	181	9						95
CLGLSYDGLL	181	10						96
CQDFFPVI	143	8						97
DLESEFQA	100	8						98
DLESEFQAA	100	9						99
DLESEFQAAI	100	10						100
DLVQENYL	249	8						101
EALGLVGA	21	8						102
EALGLVGAQA	21	10						103
EARGEALGL	17	9						104
EARGEALGLV	17	10						105
ELVHFLLL	115	8						106
EQQTASSSST	35	10						107
EQQTASSSSTL	35	11						108
ETSYVKVL	280	8						109
ETSYVKVLHHT	280	11						110
EVFEGREDSV	229	10						111
EVTLGEVPA	47	9						112
EVTLGEVPAA	47	10						113
EVVEVVPI	165	8						114
EVVEVVPISHL	165	11						115
EVVPISHL	168	8						116
EVVPISHLYI	168	10						117
EVVPISHLYIL	168	11						118
FAHPRKLL	239	8						119
FAHPRKLLM	239	9						120
FLLLKYRA	119	8						121
FLWGPRAL	271	8						122
FLWGPRALI	271	9						123
FLWGPRALIET	271	11						124
FQAAISRKM	105	9						125
FQAAISRKMV	105	10						126

Table VIII A
Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
GASSFSTT	67	8						127
GASSFSTTI	67	9						128
GIEVVEVV	163	8						129
GIEVVEVVPI	163	10						130
GLEARGEA	15	8						131
GLEARGEAL	15	9						132
GLEARGEALGL	15	11						133
GLLGDNQV	188	8						134
GLLGDNQVM	188	9						135
GLLIIVLA	200	8						136
GLLIIVLAI	200	9						137
GLLIIVLAII	200	10						138
GLLIIVLAIIA	200	11						139
GLSYDGLL	183	8						140
GLVGAQAPA	24	9						141
GLVGAQAPAT	24	10						142
HISYPPLHERA	298	11						143
HLYILVTCL	174	9						144
HLYILVTCLGL	174	11						145
HTLKIGGEPHI	289	11						146
IAIEGDCA	209	8						147
IIAIEGDCA	208	9						148
IIVLAIIA	203	8						149
IIVLAIIAI	203	9						150
ILVTCLGL	177	8						151
IVLAIIAI	204	8						152
KAEMLESV	132	8						153
KAEMLESVL	132	9						154
KASEYLQL	153	8						155
KASEYLQLV	153	9						156
KIGGEPHI	292	8						157
KIWEELSM	220	8						158
KIWEELSML	220	9						159
KIWEELSMLEV	220	11						160
KLLMQDLV	244	8						161
KMVELVHFL	112	9						162
KMVELVHFLL	112	10						163
KMVELVHFLLL	112	11						164
KTGLLIIV	198	8						165
KTGLLIIVL	198	9						166
KTGLLIIVLA	198	10						167
KTGLLIIVLAI	198	11						168
KVLHHTLKI	285	9						169
LAIIAIEGDCA	206	11						170
LIETSYVKV	278	9						171
LIETSYVKVL	278	10						172

Table VIII A

Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
LIIVLAII	202	8						173
LIIVLAIIA	202	9						174
LIIVLAIIAI	202	10						175
LLGDNQVM	189	8						176
LLGDNQVMPKT	189	11						177
LLIIVLAI	201	8						178
LLIIVLAII	201	9						179
LLIIVLAIIA	201	10						180
LLIIVLAIIAI	201	11						181
LLKYRAREPV	121	10						182
LLKYRAREPVT	121	11						183
LLLKYRAREPV	120	11						184
LMQDLVQENYL	246	11						185
LQLVFGIEV	158	9						186
LQLVFGIEVV	158	10						187
LVEVTLGEV	45	9						188
LVEVTLGEVPA	45	11						189
LVFGIEVV	160	8						190
LVFGIEVVEV	160	10						191
LVFGIEVVEVV	160	11						192
LVGAQAPA	25	8						193
LVGAQAPAT	25	9						194
LVHFLLLKYRA	116	11						195
MQDLVQENYL	247	10						196
MVELVHFL	113	8						197
MVELVHFLL	113	9						198
MVELVHFLLL	113	10						199
NQEEEGPRM	89	9						200
NQVMPKTGL	193	9						201
NQVMPKTGLL	193	10						202
NQVMPKTGLLI	193	11						203
PATEEQQT	31	8						204
PATEEQQTA	31	9						205
PISHLYIL	171	8						206
PISHLYILV	171	9						207
PISHLYILVT	171	10						208
PQGASSFST	65	9						209
PQGASSFSTT	65	10						210
PQGASSFSTTI	65	11						211
PVIFSKASEYL	148	11						212
PVTKAEML	129	8						213
PVTKAEMLESV	129	11						214
QAAISRKM	106	8						215
QAAISRKMV	106	9						216
QAAISRKMVEL	106	11						217
QAPATEEQQT	29	10						218

Table VIII A

Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
QAPATEEQQTA	29	11						219
QLVFGIEV	159	8						220
QLVFGIEVV	159	9						221
QLVFGIEVVEV	159	11						222
QQTASSSST	36	9						223
QQTASSSSTL	36	10						224
QQTASSSSTLV	36	11						225
QTASSSST	37	8						226
QTASSSSTL	37	9						227
QTASSSSTLV	37	10						228
QVMPKTGL	194	8						229
QVMPKTGLL	194	9						230
QVMPKTGLLI	194	10						231
QVMPKTGLLII	194	11						232
QVPGSDPA	260	8						233
RALIETSYV	276	9						234
RALIETSYVKV	276	11						235
RAREPVTKA	125	9						236
RAREPVTKAEM	125	11						237
RQVPGSDPA	259	9						238
SQHCKPEEGL	7	10						239
STLVEVTL	43	8						240
STLVEVTLGEV	43	11						241
STTINYTL	72	8						242
SVFAHPRKL	237	9						243
SVFAHPRKLL	237	10						244
SVFAHPRKLLM	237	11						245
TASSSSTL	38	8						246
TASSSSTLV	38	9						247
TASSSSTLVEV	38	11						248
TLGEVPAA	49	8						249
TLKIGGEPHI	290	10						250
TLVEVTLGEV	44	10						251
VIFSKASEYL	149	10						252
VLHHTLKI	286	8						253
VLRNCQDFFPV	139	11						254
VMPKTGLL	195	8						255
VMPKTGLLI	195	9						256
VMPKTGLLII	195	10						257
VMPKTGLLIIV	195	11						258
VQENYLEYRQV	251	11						259
VTCLGLSYDGL	179	11						260
VTKAEMLESV	130	10						261
VTKAEMLESVL	130	11						262
VTLGEVPA	48	8						263
VTLGEVPAA	48	9						264

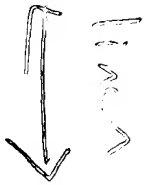

Table VIII A

Mage 2 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
VVEVVPISHL	166	10						265
VVPISHLYI	169	9						266
VVPISHLYIL	169	10						267
VVPISHLYILV	169	11						268
YILVTCLGL	176	9						269
YLQLVFGI	157	8						270
YLQLVFGIEV	157	10						271
YLQLVFGIEVV	157	11						272
YVKVLHHT	283	8						273
YVKVLHHTL	283	9						274
YVKVLHHTLKI	283	11						275

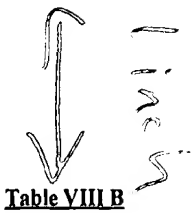

Table VIII B

Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
AALSRKVA	107	8						276
AALSRKVAEL	107	10	0.0007					277
AALSRKVAELV	107	11						278
AASSSSTL	38	8						279
AASSSSTLV	38	9	0.0001					280
AASSSSTLVEV	38	11						281
AIIAREGDCA	207	10	0.0002					282
ALGLVGAQA	22	9	0.0030					283
ALGLVGAQAPA	22	11						284
ALSRKVAEL	108	9	0.0050					285
ALSRKVAELV	108	10	0.0001					286
ALVETSYV	277	8						287
ALVETSYVKV	277	10	0.0024					288
ALVETSYVKVL	277	11						289
AQAPATEEQEA	28	11						290
ATCLGLSYDGL	179	11						291
ATEEQEAA	32	8						292
CAPEEKIWEEL	215	11						293
CLGLSYDGL	181	9	0.0004					294
CLGLSYDGLL	181	10	0.0001					295
DLESEFQA	100	8						296
DLESEFQAA	100	9	0.0001					297
DLESEFQAAL	100	10	0.0001					298
EAASSSST	37	8						299
EAASSSSTL	37	9	0.0001					300
EAASSSSTLV	37	10	0.0001					301
EALGLVGA	21	8						302
EALGLVGAQA	21	10	0.0001					303
EARGEALGL	17	9	0.0001					304
EARGEALGLV	17	10	0.0001					305
ELMEVDPI	165	8						306
ELMEVDPIGHL	165	11	0.0260					307
ELVHFLLL	115	8						308
EQEAASSSST	35	10						309
EQEAASSSSTL	35	11						310
ETSYVKVL	280	8						311
ETSYVKVLHHM	280	11						312
EVDPIGHL	168	8						313
EVDPIGHLYI	168	10	0.0002					314
EVFEGREDSI	229	10	0.0001					315
EVFEGREDSIL	229	11						316
EVTLGEVPA	47	9	0.0001					317
EVTLGEVPAA	47	10	0.0001					318
FLLLKYRA	119	8						319
FLWGPRAL	271	8						320
FLWGPRALV	271	9	0.0820	0.0500	0.9100	0.0043	1.1000	321
FLWGPRALVET	271	11						322
FQAALSRKV	105	9						323

Table VIII B

Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
FQAALSRKVA	105	10						324
GASSLPTT	67	8						325
GASSLPTTM	67	9	0.0001					326
GIELMEVDPI	163	10	0.0002					327
GLEARGEA	15	8						328
GLEARGEAL	15	9	0.0001					329
GLEARGEALGL	15	11						330
GLLGDNQI	188	8						331
GLLGDNQIM	188	9						332
GLLIIVLA	200	8						333
GLLIIVLAI	200	9	0.0002					334
GLLIIVLAII	200	10	0.0005					335
GLLIIVLAIIA	200	11						336
GLSYDGLL	183	8						337
GLVGAQAPA	24	9	0.0003					338
GLVGAQAPAT	24	10	0.0004					339
HISYPPLHEWV	298	11						340
HLYIFATCL	174	9	0.0003					341
HLYIFATCLGL	174	11	0.0410	0.0140	0.1500	0.0029	0.1500	342
HMVKISGGPHI	289	11						343
IAREGDCA	209	8						344
IIAREGDCA	208	9	0.0001					345
IIVLAIIA	203	8						346
ILGDPKKL	238	8						347
ILGDPKKLL	238	9	0.0001					348
ILGDPKKLLT	238	10	0.0001					349
IMPKAGLL	195	8						350
IMPKAGLLI	195	9	0.0064					351
IMPKAGLLII	195	10	0.0015					352
IMPKAGLLIIV	195	11	0.0130					353
KAEMLGSV	132	8						354
KAEMLGSVV	132	9	0.0001					355
KAGLLIIV	198	8						356
KAGLLIIVL	198	9	0.0002					357
KAGLLIIVLA	198	10	0.0002					358
KAGLLIIVLAI	198	11						359
KASSSLQL	153	8						360
KASSSLQLV	153	9	0.0005					361
KISGGPHI	292	8						362
KIWEELSV	220	8						363
KIWEELSVL	220	9	0.0140	0.0064	0.0073	0.0590	0.0012	364
KIWEELSVLEV	220	11						365
KLLTQHFV	244	8						366
KVAELVHFL	112	9	0.0550					367
KVAELVHFLL	112	10	0.0120					368
KVAELVHFLLL	112	11						369
KVLHHMVKI	285	9	0.0026					370
LAIIAREGDCA	206	11						371

Table VIII B

Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
LIIVLAII	202	8						372
LIIVLAIIA	202	9	0.0008					373
LLGDNQIM	189	8						374
LLGDNQIMPKA	189	11						375
LLIIVLAI	201	8						376
LLIIVLAII	201	9	0.0001					377
LLIIVLAIIA	201	10	0.0002					378
LLKYRAREPV	121	10	0.0001					379
LLKYRAREPVT	121	11						380
LLLKYRAREPV	120	11	0.0001					381
LMEVDPIGHL	166	10	0.0005					382
LQLVFGIEL	158	9						383
LQLVFGIELM	158	10						384
LTQHFVQENYL	246	11						385
LVETSYVKV	278	9	0.0001					386
LVETSYVKVL	278	10	0.0002					387
LVEVTLGEV	45	9	0.0001					388
LVEVTLGEVPA	45	11						389
LVFGIELM	160	8						390
LVFGIELMEV	160	10	0.1100					391
LVGAQAPA	25	8						392
LVGAQAPAT	25	9	0.0001					393
LVHFLLLKYRA	116	11						394
MVKISGGPHI	290	10	0.0002					395
NQEEEGPST	89	9						396
NQIMPKAGL	193	9						397
NQIMPKAGLL	193	10						398
NQIMPKAGLLI	193	11						399
PATEEQEA	31	8						400
PATEEQEAA	31	9	0.0001					401
PIGHLYIFA	171	9	0.0001					402
PIGHLYIFAT	171	10	0.0003					403
PQGASSLPT	65	9						404
PQGASSLPTT	65	10						405
PQGASSLPTTM	65	11						406
PQSPQGASSL	62	10						407
PTTMNYPL	72	8						408
PVIFSKASSSL	148	11						409
PVTKAEML	129	8						410
PVTKAEMLGSV	129	11						411
QAALSRKV	106	8						412
QAALSRKVA	106	9	0.0001					413
QAALSRKVAEL	106	11						414
QAPATEEQEA	29	10	0.0001					415
QAPATEEQEAA	29	11						416
QIMPKAGL	194	8						417
QIMPKAGLL	194	9	0.0001					418
QIMPKAGLLI	194	10	0.0006					419

Table VIII B

Mage 3 A02 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO.
QIMPKAGLLII	194	11						420
QLVFGIEL	159	8						421
QLVFGIELM	159	9	0.0010					422
QLVFGIELMEV	159	11	0.3400					423
QVPGSDPA	260	8						424
RALVETSYV	276	9	0.0001					425
RALVETSYVKV	276	11						426
RAREPVTKA	125	9						427
RAREPVTKAEM	125	11						428
RQVPGSDPA	259	9						429
SILGDPKKL	237	9	0.0001					430
SILGDPKKLL	237	10	0.0002					431
SILGDPKKLLT	237	11						432
SLPTTMNYPL	70	10	0.0035					433
SLQLVFGI	157	8						434
SLQLVFGIEL	157	10	0.0049					435
SLQLVFGIELM	157	11						436
SQHCKPEEGL	7	10						437
STLVEVTL	43	8						438
STLVEVTLGEV	43	11	0.0140					439
TLGEVPAA	49	8						440
TLVEVTLGEV	44	10	0.0250	0.0320	1.6000	0.0039	0.1600	441
TQHFVQENYL	247	10						442
VAELVHFL	113	8						443
VAELVHFLL	113	9	0.0001					444
VAELVHFLLL	113	10	0.0009					445
VIFSKASSSL	149	10	0.0001					446
VLHHMVKI	286	8						447
VQENYLEYRQV	251	11						448
VTKAEMLGSV	130	10	0.0002					449
VTKAEMLGSVV	130	11						450
VTLGEVPA	48	8						451
VTLGEVPAA	48	9	0.0045					452
VVGNWQYFFPV	139	11						453
WQYFFPVI	143	8						454
YIFATCLGL	176	9	0.0180					455
YVKVLHHM	283	8						456
YVKVLHHMV	283	9	0.0001					457
YVKVLHHMVKI	283	11						458

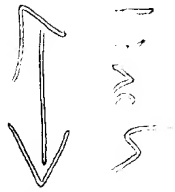

Table IX a

Mage 2 A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
AIEGDCAPEEK	210	11	0.0009	0.0007				459
ALIETSYVK	277	9	0.0810	0.1900	0.0200	0.0003	0.0280	460
DLVQENYLEYR	249	11	0.0047	0.0018				461
DSVFAHPR	236	8	-0.0004	0.0005				462
DSVFAHPRK	236	9	0.0021	0.0025	0.0006	0.0190	0.0460	463
ELSMLEVFEGR	224	11	0.0016	0.0008				464
ELVHFLLLK	115	9	0.0045	0.0011				465
ELVHFLLLKYR	115	11	0.0011	0.0031				466
EMLESVLR	134	8	-0.0009	-0.0003				467
ESEFQAAISR	102	10	0.0002	0.0002				468
ESEFQAAISRK	102	11	0.0010	0.0004				469
FLLLKYRAR	119	9						470
FSTTINYTLWR	71	11	0.0110	0.0170	0.0700	0.0074	0.0490	471
GLLGDNQVMPK	188	11	0.0780	0.0047	-0.0006	-0.0013	-0.0001	472
GSSNQEEEGPR	86	11	-0.0002	-0.0002				473
HISYPPLHER	298	10	0.0074	0.0018				474
ISYPPLHER	299	9	0.0340	0.0280	0.7700	0.8100	0.0990	475
KAEMLESVLR	132	10	0.0002	0.0009	0.0084	0.0047	0.0004	476
KVLHHTLK	285	8	0.0053	0.0100				477
LIETSYVK	278	8	-0.0004	0.0027				478
LLGDNQVMPK	189	10	0.0093	0.0014				479
LLLKYRAR	120	8	-0.0009	-0.0004				480
LSMLEVFEGR	225	10	-0.0004	0.0001				481
LVHFLLLK	116	8	0.0290	0.1500	0.0007	-0.0009	0.0200	482
LVHFLLLKYR	116	10	0.0260	0.0022				483
LVQENYLEYR	250	10	0.0027	0.0089				484
MLEVFEGR	227	8	-0.0009	-0.0004				485
MVELVHFLLLK	113	11	0.0200	0.0120	0.0038	0.0056	0.0220	486
PACYEFLWGPR	266	11	-0.0009	-0.0002				487
PLEQRSQHCK	2	10	0.0003	0.0002				488
PLHERALR	303	8	-0.0009	-0.0004				489
RALIETSYVK	276	10	0.0200	0.0750	0.0064	0.0003	0.0026	490
RAREPVTK	125	8	-0.0009	-0.0003				491
SMLEVFEGR	226	9	0.0020	0.0220	0.4900	3.2000	0.0044	492
SSNQEEEGPR	87	10	0.0002	0.0002				493
STTINYTLWR	72	10	0.0014	0.0910				494
SVFAHPRK	237	8	0.1410	0.0810	0.0130	0.0010	0.0440	495
TINYTLWR	74	8	0.0140	0.0550	0.0250	0.0370	0.3800	496
TTINYTLWR	73	9	0.0890	1.1000				497
YVKVLHHTLK	283	10	0.0033	0.0160	0.0005	-0.0009	0.0360	498

Table IX B

Mage 3 A03 Supermotif with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO.
ALVETSYVK	277	9	0.0270	0.1700	0.0009	0.0004	0.0022	499
DSILGDPK	236	8	-0.0004	-0.0003				500
DSILGDPKK	236	9	-0.0003	-0.0002				501
ELSVLEVFEGR	224	11	-0.0009	0.0023				502
ELVHFLLLK	115	9	0.0045	0.0011				503
ELVHFLLLKYR	115	11	0.0011	0.0031				504
ESEFQAALSR	102	10	0.0002	0.0002				505
ESEFQAALSRK	102	11	0.0002	0.0004				506
FLLLKYRAR	119	9						507
FVQENYLEYR	250	10	0.0009	0.0012				508
GLLGDNQIMPK	188	11	0.1300	0.0570	-0.0006	-0.0013	-0.0001	509
IIVLAIIAR	203	9	0.0069	0.0011				510
IVLAIIAR	204	8	0.0053	0.0037				511
KVLHHMVK	285	8	0.0580	0.0190	0.0012	0.0052	-0.0001	512
LIIVLAIIAR	202	10	0.0280	0.0021				513
LLGDNQIMPK	189	10	0.0200	0.0110				514
LLIIVLAIIAR	201	11	0.0021	0.0056				515
LLLKYRAR	120	8	-0.0009	-0.0004				516
LSVLEVFEGR	225	10	-0.0006	0.0030				517
LVETSYVK	278	8	-0.0004	0.0014				518
LVHFLLLK	116	8	0.0290	0.1500	0.0007	-0.0009	0.0200	519
LVHFLLLKYR	116	10	0.0260	0.0022				520
PACYEFLWGPR	266	11	-0.0009	-0.0002				521
PLEQRSQHCK	2	10	0.0003	0.0002				522
PLHEWVLR	303	8	-0.0009	-0.0003				523
RALVETSYVK	276	10	0.0190	0.1100	0.0034	0.0003	0.0004	524
RAREPVTK	125	8	-0.0009	-0.0003				525
SILGDPKK	237	8	-0.0009	0.0012				526
SVLEVFEGR	226	9	0.0003	0.1400	0.1700	0.6600	0.0860	527
VAELVHFLLLK	113	11	-0.0002	0.0011				528
VLEVFEGR	227	8	0.0016	0.0005				529
YVKVLHHMVK	283	10	0.0020	0.0061				530

Table X A

Mage 2 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
AISRKMVEL	108	9		531
ALIETSYVKVL	277	11		532
CLGLSYDGL	181	9		533
CLGLSYDGLL	181	10		534
CYEFLWGPRAL	268	11	0.0004	535
DLESEFQAAI	100	10		536
DLVQENYL	249	8		537
DLVQENYLEY	249	10		538
EFLWGPRAL	270	9	0.0006	539
EFLWGPRALI	270	10	0.0097	540
EFQAAISRKM	104	10	0.0002	541
ELSMLEVF	224	8		542
ELVHFLLL	115	8		543
ELVHFLLLKY	115	10		544
ETSYVKVL	280	8		545
EVFEGREDSVF	229	11		546
EVVEVVPI	165	8		547
EVVEVVPISHL	165	11		548
EVVPISHL	168	8		549
EVVPISHLY	168	9		550
EVVPISHLYI	168	10		551
EVVPISHLYIL	168	11		552
EYLQLVFGI	156	9	3.5000	553
FLWGPRAL	271	8		554
FLWGPRALI	271	9		555
GIEVVEVVPI	163	10		556
GLEARGEAL	15	9		557
GLEARGEALGL	15	11		558
GLLGDNQVM	188	9		559
GLLIIVLAI	200	9		560
GLLIIVLAII	200	10		561
GLSYDGLL	183	8		562
HLYILVTCL	174	9		563
HLYILVTCLGL	174	11		564
HTLKIGGEPHI	289	11		565
IFSKASEY	150	8		566
IFSKASEYL	150	9	0.0230	567
IFSKASEYLQL	150	11	0.0950	568
IIVLAIIAI	203	9		569
ILVTCLGL	177	8		570
ILVTCLGLSY	177	10		571
IVLAIIAI	204	8		572
IWEELSML	221	8	0.0007	573
IWEELSMLEVF	221	11	0.0170	574
KIGGEPHI	292	8		575
KIGGEPHISY	292	10		576

Table X A

Mage 2 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
KIWEELSM	220	8		577
KIWEELSML	220	9		578
KMVELVHF	112	8	0.0005	579
KMVELVHFL	112	9		580
KMVELVHFLL	112	10		581
KMVELVHFLLL	112	11		582
KTGLLIIVL	198	9		583
KTGLLIIVLAI	198	11		584
KVLHHTLKI	285	9		585
LIETSYVKVL	278	10		586
LIIVLAII	202	8		587
LIIVLAIIAI	202	10		588
LLGDNQVM	189	8		589
LLIIVLAI	201	8		590
LLIIVLAII	201	9		591
LLIIVLAIIAI	201	11		592
LLMQDLVQENY	245	11		593
LMQDLVQENY	246	10		594
LMQDLVQENYL	246	11		595
LVHFLLLKY	116	9		596
LVQENYLEY	250	9		597
LVTCLGLSY	178	9		598
LWGPRALI	272	8	0.1200	599
LYILVTCL	175	8	0.0086	600
LYILVTCLGL	175	10	0.0140	601
MFPDLESEF	97	9	0.0140	602
MVELVHFL	113	8		603
MVELVHFLL	113	9		604
MVELVHFLLL	113	10		605
PISHLYIL	171	8		606
PVIFSKASEY	148	10		607
PVIFSKASEYL	148	11		608
PVTKAEML	129	8		609
QTASSSSTL	37	9		610
QVMPKTGL	194	8		611
QVMPKTGLL	194	9		612
QVMPKTGLLI	194	10		613
QVMPKTGLLII	194	11		614
QVPGSDPACY	260	10		615
RMFPDLESEF	96	10	0.0016	616
SFSTTINY	70	8		617
SFSTTINYTL	70	10	0.0150	618
SFSTTINYTLW	70	11	0.0280	619
STLVEVTL	43	8		620
STTINYTL	72	8		621
STTINYTLW	72	9		622

Table X A

Mage 2_A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
SVFAHPRKL	237	9		623
SVFAHPRKLL	237	10		624
SVFAHPRKLLM	237	11		625
SVLRNCQDF	138	9		626
SVLRNCQDFF	138	10		627
SYPPLHERAL	300	10	0.0003	628
SYVKVLHHTL	282	10	0.1600	629
TLKIGGEPHI	290	10		630
TTINYTLW	73	8		631
VFAHPRKL	238	8	0.0005	632
VFAHPRKLL	238	9	0.0006	633
VFAHPRKLLM	238	10		634
VFEGREDSVF	230	10	0.0004	635
VIFSKASEY	149	9		636
VIFSKASEYL	149	10		637
VLHHTLKI	286	8		638
VLRNCQDF	139	8		639
VLRNCQDFF	139	9		640
VMPKTGLL	195	8	-0.0004	641
VMPKTGLLI	195	9	0.2300	642
VMPKTGLLII	195	10	0.0580	643
VTCLGLSY	179	8		644
VTCLGLSYDGL	179	11		645
VTKAEMLESVL	130	11		646
VVEVVPISHL	166	10		647
VVEVVPISHLY	166	11		648
VVPISHLY	169	8		649
VVPISHLYI	169	9		650
VVPISHLYIL	169	10		651
YILVTCLGL	176	9		652
YILVTCLGLSY	176	11		653
YLQLVFGI	157	8		654
YVKVLHHTL	283	9		655
YVKVLHHTLKI	283	11		656

Table X B

Mage 3 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
ALSRKVAEL	108	9		657
ALVETSYVKVL	277	11		658
ATCLGLSY	179	8		659
ATCLGLSYDGL	179	11		660
CLGLSYDGL	181	9		661
CLGLSYDGLL	181	10		662
CYEFLWGPRAL	268	11	0.0004	663
DLESEFQAAL	100	10		664
EFLWGPRAL	270	9	0.0006	665
ELMEVDPI	165	8		666
ELMEVDPIGHL	165	11		667
ELSVLEVF	224	8		668
ELVHFLLL	115	8		669
ELVHFLLLKY	115	10		670
EMLGSVVGNW	134	10	0.0017	671
ETSYVKVL	280	8		672
ETSYVKVLHHM	280	11		673
EVDPIGHL	168	8		674
EVDPIGHLY	168	9		675
EVDPIGHLYI	168	10		676
EVDPIGHLYIF	168	11		677
EVFEGREDSI	229	10		678
EVFEGREDSIL	229	11		679
FLWGPRAL	271	8		680
FVQENYLEY	250	9		681
GIELMEVDPI	163	10		682
GLEARGEAL	15	9		683
GLEARGEALGL	15	11		684
GLLGDNQI	188	8		685
GLLGDNQIM	188	9		686
GLLIIVLAI	200	9		687
GLLIIVLAII	200	10		688
GLSYDGLL	183	8		689
HFVQENYL	249	8	-0.0004	690
HFVQENYLEY	249	10		691
HISYPPLHEW	298	10		692
HLYIFATCL	174	9		693
HLYIFATCLGL	174	11		694
HMVKISGGPHI	289	11		695
IFATCLGL	177	8	0.0120	696
IFATCLGLSY	177	10		697
IFSKASSSL	150	9	0.0160	698
IFSKASSSLQL	150	11	0.0910	699
ILGDPKKL	238	8		700
ILGDPKKLL	238	9		701

Table X B

Mage 3 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
IMPKAGLL	195	8		702
IMPKAGLLI	195	9	0.4200	703
IMPKAGLLII	195	10	0.0500	704
IWEELSVL	221	8	-0.0004	705
IWEELSVLEVF	221	11	0.0260	706
KISGGPHI	292	8		707
KISGGPHISY	292	10		708
KIWEELSVL	220	9		709
KVAELVHF	112	8		710
KVAELVHFL	112	9		711
KVAELVHFLL	112	10		712
KVAELVHFLLL	112	11		713
KVLHHMVKI	285	9		714
LIIVLAII	202	8		715
LLGDNQIM	189	8		716
LLIIVLAI	201	8		717
LLIIVLAII	201	9		718
LLTQHFVQENY	245	11		719
LMEVDPIGHL	166	10		720
LMEVDPIGHLY	166	11		721
LTQHFVQENY	246	10		722
LTQHFVQENYL	246	11		723
LVETSYVKVL	278	10		724
LVFGIELM	160	8		725
LVHFLLLKY	116	9		726
LYIFATCL	175	8	0.0140	727
LYIFATCLGL	175	10	0.0480	728
MLGSVVGNW	135	9		729
MLGSVVGNWQY	135	11		730
MVKISGGPHI	290	10		731
NWQYFFPVI	142	9	0.5300	732
NWQYFFPVIF	142	10	0.0170	733
NYPLWSQSY	76	9	0.0270	734
PIGHLYIF	171	8		735
PTTMNYPL	72	8		736
PTTMNYPLW	72	9		737
PVIFSKASSSL	148	11		738
PVTKAEML	129	8		739
QIMPKAGL	194	8		740
QIMPKAGLL	194	9		741
QIMPKAGLLI	194	10		742
QIMPKAGLLII	194	11		743
QLVFGIEL	159	8		744
QLVFGIELM	159	9		745
QVPGSDPACY	260	10		746

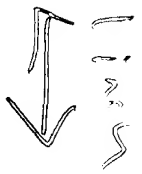

Table X B

Mage 3 A24 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
QYFFPVIF	144	8	0.1200	747
SILGDPKKL	237	9		748
SILGDPKKLL	237	10		749
SLPTTMNY	70	8		750
SLPTTMNYPL	70	10		751
SLPTTMNYPLW	70	11		752
SLQLVFGI	157	8		753
SLQLVFGIEL	157	10		754
SLQLVFGIELM	157	11		755
STFPDLESEF	96	10		756
STLVEVTL	43	8		757
SVVGNWQY	138	8		758
SVVGNWQYF	138	9		759
SVVGNWQYFF	138	10		760
SYDGLLGDNQI	185	11	0.0026	761
SYPPLHEW	300	8	0.0420	762
SYPPLHEWVL	300	10	0.5900	763
SYVKVLHHM	282	9		764
TFPDLESEF	97	9	0.0049	765
TMNYPLWSQSY	74	11		766
TTMNYPLW	73	8		767
VFEGREDSI	230	9	-0.0004	768
VFEGREDSIL	230	10	-0.0005	769
VIFSKASSSL	149	10		770
VLHHMVKI	286	8		771
VVGNWQYF	139	8		772
VVGNWQYFF	139	9		773
YIFATCLGL	176	9		774
YIFATCLGLSY	176	11		775
YVKVLHHM	283	8		776
YVKVLHHMVKI	283	11		777

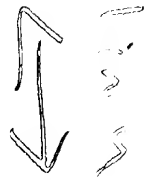

Table XI A

Mage 2 B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
APATEEQQTA	30	10	0.0002	778
APEEKIWEEL	216	10	0.0001	779
DPACYEFL	265	8	-0.0002	780
DPACYEFLW	265	9	0.0001	781
EPHISYPPL	296	9	0.1100	782
EPVTKAEM	128	8	0.0010	783
EPVTKAEML	128	9	0.0001	784
FPDLESEF	98	8	-0.0002	785
FPDLESEFQA	98	10	0.0002	786
FPDLESEFQAA	98	11	-0.0001	787
FPVIFSKA	147	8	0.0003	788
FPVIFSKASEY	147	11	0.0004	789
GPRALIETSY	274	10	0.0008	790
GPRALIETSYV	274	11	0.1300	791
GPRMFPDL	94	8	0.0063	792
HPRKLLMQDL	241	10	0.0400	793
HPRKLLMQDLV	241	11	0.0042	794
KPEEGLEA	11	8	-0.0002	795
MPKTGLLI	196	8	0.0190	796
MPKTGLLII	196	9	0.0020	797
MPKTGLLIIV	196	10	0.0003	798
MPKTGLLIIVL	196	11	0.0099	799
PPHSPQGA	61	8	-0.0002	800
PPHSPQGASSF	61	11	-0.0003	801
PPLHERAL	302	8	0.0026	802
SPPHSPQGA	60	9	0.0001	803
SPQGASSF	64	8	0.0007	804
SPSPPHSPQGA	58	11	0.0006	805
VPGSDPACY	261	9	0.0001	806
VPGSDPACYEF	261	11	-0.0001	807
VPISHLYI	170	8	0.0170	808
VPISHLYIL	170	9	0.2500	809
VPISHLYILV	170	10	0.0027	810
YPPLHERA	301	8	-0.0002	811
YPPLHERAL	301	9	0.2700	812

Table XI B

Mage 3 B07 Supermotif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	B*0702	SEQ ID NO.
APATEEQEA	30	9	0.0001	813
APATEEQEAA	30	10	0.0002	814
APEEKIWEEL	216	10	0.0001	815
DPACYEFL	265	8	-0.0002	816
DPACYEFLW	265	9	0.0001	817
DPIGHLYI	170	8	-0.0002	818
DPIGHLYIF	170	9	0.0001	819
DPIGHLYIFA	170	10	0.0002	820
DPKKLLTQHF	241	10	0.0001	821
DPKKLLTQHFV	241	11	-0.0004	822
DPPQSPQGA	60	9	0.0001	823
EPVTKAEM	128	8	0.0010	824
EPVTKAEML	128	9	0.0001	825
FPDLESEF	98	8	-0.0002	826
FPDLESEFQA	98	10	0.0002	827
FPDLESEFQAA	98	11	-0.0001	828
FPVIFSKA	147	8	0.0003	829
GPHISYPPL	296	9	0.8800	830
GPRALVETSY	274	10	0.0002	831
GPRALVETSYV	274	11	0.1900	832
GPSTFPDL	94	8	-0.0002	833
KPEEGLEA	11	8	-0.0002	834
LPTTMNYPL	71	9	0.0770	835
LPTTMNYPLW	71	10	0.0001	836
MPKAGLLI	196	8	0.1300	837
MPKAGLLII	196	9	0.0170	838
MPKAGLLIIV	196	10	0.0031	839
MPKAGLLIIVL	196	11	0.0280	840
PPLHEWVL	302	8	-0.0002	841
PPQSPQGA	61	8	-0.0002	842
PPQSPQGASSL	61	11	0.0049	843
SPDPPQSPQGA	58	11	-0.0001	844
SPQGASSL	64	8	0.0081	845
VPGSDPACY	261	9	0.0001	846
VPGSDPACYEF	261	11	-0.0001	847
YPLWSQSY	77	8	-0.0002	848
YPPLHEWV	301	8	-0.0002	849
YPPLHEWVL	301	9	0.0027	850

Table XII A

Mage 2 B27 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AHPRKLLM	240	8	851
AHPRKLLMQDL	240	11	852
AREPVTKAEM	126	10	853
AREPVTKAEML	126	11	854
ARGEALGL	18	8	855
EKIWEELSM	219	9	856
EKIWEELSML	219	10	857
LKIGGEPHI	291	9	858
LKIGGEPHISY	291	11	859
LRNCQDFF	140	8	860
LRNCQDFFPVI	140	11	861
PHISYPPL	297	8	862
PHSPQGASSF	62	10	863
PKTGLLII	197	8	864
PKTGLLIIVL	197	10	865
PRALIETSY	275	9	866
PRKLLMQDL	242	9	867
PRMFPDLESEF	95	11	868
QHCKPEEGL	8	9	869
RKLLMQDL	243	8	870
RKMVELVHF	111	9	871
RKMVELVHFL	111	10	872
RKMVELVHFLL	111	11	873
SHLYILVTCL	173	10	874
SKASEYLQL	152	9	875
SKASEYLQLVF	152	11	876
SRKMVELVHF	110	10	877
SRKMVELVHFL	110	11	878
TKAEMLESVL	131	10	879
VHFLLLKY	117	8	880
VKVLHHTL	284	8	881
VKVLHHTLKI	284	10	882

Table XII B

Mage 3 B27 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AREPVTKAEM	126	10	883
AREPVTKAEML	126	11	884
ARGEALGL	18	8	885
EKIWEELSVL	219	10	886
GHLYIFATCL	173	10	887
KKLLTQHF	243	8	888
PHISYPPL	297	8	889
PHISYPPLHEW	297	11	890
PKAGLLII	197	8	891
PKAGLLIIVL	197	10	892
PKKLLTQHF	242	9	893
PRALVETSY	275	9	894
QHCKPEEGL	8	9	895
QHFVQENY	248	8	896
QHFVQENYL	248	9	897
QHFVQENYLEY	248	11	898
RKVAELVHF	111	9	899
RKVAELVHFL	111	10	900
RKVAELVHFLL	111	11	901
SKASSSLQL	152	9	902
SKASSSLQLVF	152	11	903
SRKVAELVHF	110	10	904
SRKVAELVHFL	110	11	905
VHFLLLKY	117	8	906
VKISGGPHI	291	9	907
VKISGGPHISY	291	11	908
VKVLHHMVKI	284	10	909

Table XIIIA
Mage 2 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AAISRKMV	107	8	910
AAISRKMVEL	107	10	911
AAISRKMVELV	107	11	912
ASEYLQLV	154	8	913
ASEYLQLVF	154	9	914
ASEYLQLVFGI	154	11	915
ASSFSTTI	68	8	916
ASSFSTTINY	68	10	917
ASSSSTLV	39	8	918
ASSSSTLVEV	39	10	919
CAPEEKIW	215	8	920
CAPEEKIWEEL	215	11	921
DSVFAHPRKL	236	10	922
DSVFAHPRKLL	236	11	923
EARGEALGL	17	9	924
EARGEALGLV	17	10	925
ESEFQAAI	102	8	926
ESVLRNCQDF	137	10	927
ESVLRNCQDFF	137	11	928
ETSYVKVL	280	8	929
FAHPRKLL	239	8	930
FAHPRKLLM	239	9	931
FSKASEYL	151	8	932
FSKASEYLQL	151	10	933
FSKASEYLQLV	151	11	934
FSTTINYTL	71	9	935
FSTTINYTLW	71	10	936
GASSFSTTI	67	9	937
GASSFSTTINY	67	11	938
GSDPACYEF	263	9	939
GSDPACYEFL	263	10	940
GSDPACYEFLW	263	11	941
HSPQGASSF	63	9	942
HTLKIGGEPHI	289	11	943
ISHLYILV	172	8	944
ISHLYILVTCL	172	11	945
ISRKMVEL	109	8	946
ISRKMVELV	109	9	947
ISRKMVELVHF	109	11	948
ISYPPLHERAL	299	11	949
KAEMLESV	132	8	950
KAEMLESVL	132	9	951
KASEYLQL	153	8	952
KASEYLQLV	153	9	953
KASEYLQLVF	153	10	954
KTGLLIIV	198	8	955

Table XIII A
Mage 2 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
KTGLLIIVL	198	9	956
KTGLLIIVLAI	198	11	957
PACYEFLW	266	8	958
QAAISRKM	106	8	959
QAAISRKMV	106	9	960
QAAISRKMVEL	106	11	961
QTASSSSTL	37	9	962
QTASSSSTLV	37	10	963
RALIETSY	276	8	964
RALIETSYV	276	9	965
RALIETSYVKV	276	11	966
RAREPVTKAEM	125	11	967
RSQHCKPEEGL	6	11	968
SSFSTTINY	69	9	969
SSFSTTINYTL	69	11	970
SSNQEEEGPRM	87	11	971
SSSSTLVEV	40	9	972
SSSSTLVEVTL	40	11	973
SSSTLVEV	41	8	974
SSSTLVEVTL	41	10	975
SSTLVEVTL	42	9	976
STLVEVTL	43	8	977
STLVEVTLGEV	43	11	978
STTINYTL	72	8	979
STTINYTLW	72	9	980
TASSSSTL	38	8	981
TASSSSTLV	38	9	982
TASSSSTLVEV	38	11	983
TSYVKVLHHTL	281	11	984
TTINYTLW	73	8	985
VTCLGLSY	179	8	986
VTCLGLSYDGL	179	11	987
VTKAEMLESV	130	10	988
VTKAEMLESVL	130	11	989

Table XIII B

Mage 3 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AALSRKVAEL	107	10	990
AALSRKVAELV	107	11	991
AASSSSTL	38	8	992
AASSSSTLV	38	9	993
AASSSSTLVEV	38	11	994
ASSLPTTM	68	8	995
ASSLPTTMNY	68	10	996
ASSSLQLV	154	8	997
ASSSLQLVF	154	9	998
ASSSLQLVFGI	154	11	999
ASSSSTLV	39	8	1000
ASSSSTLVEV	39	10	1001
ATCLGLSY	179	8	1002
ATCLGLSYDGL	179	11	1003
CAPEEKIW	215	8	1004
CAPEEKIWEEL	215	11	1005
DSILGDPKKL	236	10	1006
DSILGDPKKLL	236	11	1007
EAASSSSTL	37	9	1008
EAASSSSTLV	37	10	1009
EARGEALGL	17	9	1010
EARGEALGLV	17	10	1011
ESEFQAAL	102	8	1012
ETSYVKVL	280	8	1013
ETSYVKVLHHM	280	11	1014
FATCLGLSY	178	9	1015
FSKASSSL	151	8	1016
FSKASSSLQL	151	10	1017
FSKASSSLQLV	151	11	1018
GASSLPTTM	67	9	1019
GASSLPTTMNY	67	11	1020
GSDPACYEF	263	9	1021
GSDPACYEFL	263	10	1022
GSDPACYEFLW	263	11	1023
GSVVGNWQY	137	9	1024
GSVVGNWQYF	137	10	1025
GSVVGNWQYFF	137	11	1026
ISGGPHISY	293	9	1027
ISYPPLHEW	299	9	1028
ISYPPLHEWV	299	10	1029
ISYPPLHEWVL	299	11	1030
KAEMLGSV	132	8	1031
KAEMLGSVV	132	9	1032
KAGLLIIV	198	8	1033
KAGLLIIVL	198	9	1034
KAGLLIIVLAI	198	11	1035

Table XIII B

Mage 3 B58 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
KASSSLQL	153	8	1036
KASSSLQLV	153	9	1037
KASSSLQLVF	153	10	1038
LSRKVAEL	109	8	1039
LSRKVAELV	109	9	1040
LSRKVAELVHF	109	11	1041
LTQHFVQENY	246	10	1042
LTQHFVQENYL	246	11	1043
PACYEFLW	266	8	1044
PSTFPDLESEF	95	11	1045
PTTMNYPL	72	8	1046
PTTMNYPLW	72	9	1047
QAALSRKV	106	8	1048
QAALSRKVAEL	106	11	1049
QSPQGASSL	63	9	1050
RALVETSY	276	8	1051
RALVETSYV	276	9	1052
RALVETSYVKV	276	11	1053
RAREPVTKAEM	125	11	1054
RSQHCKPEEGL	6	11	1055
SSLPTTMNY	69	9	1056
SSLPTTMNYPL	69	11	1057
SSLQLVFGI	156	9	1058
SSLQLVFGIEL	156	11	1059
SSSLQLVF	155	8	1060
SSSLQLVFGI	155	10	1061
SSSSTLVEV	40	9	1062
SSSSTLVEVTL	40	11	1063
SSSTLVEV	41	8	1064
SSSTLVEVTL	41	10	1065
SSTLVEVTL	42	9	1066
STFPDLESEF	96	10	1067
STLVEVTL	43	8	1068
STLVEVTLGEV	43	11	1069
TSYVKVLHHM	281	10	1070
TSYVKVLHHMV	281	11	1071
TTMNYPLW	73	8	1072
VAELVHFL	113	8	1073
VAELVHFLL	113	9	1074
VAELVHFLLL	113	10	1075
VTKAEMLGSV	130	10	1076
VTKAEMLGSVV	130	11	1077

Table XIV A

Mage 2 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
AISRKMVELV	108	10	1078
ALIETSYV	277	8	1079
ALIETSYVKV	277	10	1080
CQDFFPVI	143	8	1081
CQDFFPVIF	143	9	1082
DLESEFQAAI	100	10	1083
DLVQENYLEY	249	10	1084
DPACYEFLW	265	9	1085
ELSMLEVF	224	8	1086
ELVHFLLLKY	115	10	1087
EPVTKAEM	128	8	1088
EVFEGREDSV	229	10	1089
EVFEGREDSVF	229	11	1090
EVVEVVPI	165	8	1091
EVVPISHLY	168	9	1092
EVVPISHLYI	168	10	1093
FLWGPRALI	271	9	1094
FPDLESEF	98	8	1095
FPVIFSKASEY	147	11	1096
FQAAISRKM	105	9	1097
FQAAISRKMV	105	10	1098
GIEVVEVV	163	8	1099
GIEVVEVVPI	163	10	1100
GLLGDNQV	188	8	1101
GLLGDNQVM	188	9	1102
GLLIIVLAI	200	9	1103
GLLIIVLAII	200	10	1104
GPRALIETSY	274	10	1105
GPRALIETSYV	274	11	1106
HPRKLLMQDLV	241	11	1107
IIVLAIIAI	203	9	1108
ILVTCLGLSY	177	10	1109
IVLAIIAI	204	8	1110
KIGGEPHI	292	8	1111
KIGGEPHISY	292	10	1112
KIWEELSM	220	8	1113
KIWEELSMLEV	220	11	1114
KLLMQDLV	244	8	1115
KMVELVHF	112	8	1116
KVLHHTLKI	285	9	1117
LIETSYVKV	278	9	1118
LIIVLAII	202	8	1119
LIIVLAIIAI	202	10	1120
LLGDNQVM	189	8	1121
LLIIVLAI	201	8	1122
LLIIVLAII	201	9	1123

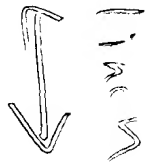

Table XIV A

Mage 2 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
LLIIVLAIIAI	201	11	1124
LLKYRAREPV	121	10	1125
LLLKYRAREPV	120	11	1126
LLMQDLVQENY	245	11	1127
LMQDLVQENY	246	10	1128
LQLVFGIEV	158	9	1129
LQLVFGIEVV	158	10	1130
LVEVTLGEV	45	9	1131
LVFGIEVV	160	8	1132
LVFGIEVVEV	160	10	1133
LVFGIEVVEVV	160	11	1134
LVHFLLLKY	116	9	1135
LVQENYLEY	250	9	1136
LVTCLGLSY	178	9	1137
MPKTGLLI	196	8	1138
MPKTGLLII	196	9	1139
MPKTGLLIIV	196	10	1140
MQDLVQENY	247	9	1141
NQEEEGPRM	89	9	1142
NQEEEGPRMF	89	10	1143
NQVMPKTGLLI	193	11	1144
PISHLYILV	171	9	1145
PPHSPQGASSF	61	11	1146
PQGASSFSTTI	65	11	1147
PVIFSKASEY	148	10	1148
PVTKAEMLESV	129	11	1149
QLVFGIEV	159	8	1150
QLVFGIEVV	159	9	1151
QLVFGIEVVEV	159	11	1152
QQTASSSSTLV	36	11	1153
QVMPKTGLLI	194	10	1154
QVMPKTGLLII	194	11	1155
QVPGSDPACY	260	10	1156
RMFPDLESEF	96	10	1157
RQVPGSDPACY	259	11	1158
SPQGASSF	64	8	1159
SVFAHPRKLLM	237	11	1160
SVLRNCQDF	138	9	1161
SVLRNCQDFF	138	10	1162
TLKIGGEPHI	290	10	1163
TLVEVTLGEV	44	10	1164
VIFSKASEY	149	9	1165
VLHHTLKI	286	8	1166
VLRNCQDF	139	8	1167
VLRNCQDFF	139	9	1168
VLRNCQDFFPV	139	11	1169

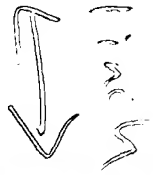

Table XIV A

Mage 2 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
VMPKTGLLI	195	9	1170
VMPKTGLLII	195	10	1171
VMPKTGLLIIV	195	11	1172
VPGSDPACY	261	9	1173
VPGSDPACYEF	261	11	1174
VPISHLYI	170	8	1175
VPISHLYILV	170	10	1176
VQENYLEY	251	8	1177
VQENYLEYRQV	251	11	1178
VVEVVPISHLY	166	11	1179
VVPISHLY	169	8	1180
VVPISHLYI	169	9	1181
VVPISHLYILV	169	11	1182
YILVTCLGLSY	176	11	1183
YLQLVFGI	157	8	1184
YLQLVFGIEV	157	10	1185
YLQLVFGIEVV	157	11	1186
YVKVLHHTLKI	283	11	1187

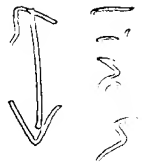

Table XIV B

Mage 3 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
ALSRKVAELV	108	10	1188
ALVETSYV	277	8	1189
ALVETSYVKV	277	10	1190
DPACYEFLW	265	9	1191
DPIGHLYI	170	8	1192
DPIGHLYIF	170	9	1193
DPKKLLTQHF	241	10	1194
DPKKLLTQHFV	241	11	1195
ELMEVDPI	165	8	1196
ELSVLEVF	224	8	1197
ELVHFLLLKY	115	10	1198
EMLGSVVGNW	134	10	1199
EPVTKAEM	128	8	1200
EVDPIGHLY	168	9	1201
EVDPIGHLYI	168	10	1202
EVDPIGHLYIF	168	11	1203
EVFEGREDSI	229	10	1204
FLWGPRALV	271	9	1205
FPDLESEF	98	8	1206
FQAALSRKV	105	9	1207
FVQENYLEY	250	9	1208
GIELMEVDPI	163	10	1209
GLLGDNQI	188	8	1210
GLLGDNQIM	188	9	1211
GLLIIVLAI	200	9	1212
GLLIIVLAII	200	10	1213
GPRALVETSY	274	10	1214
GPRALVETSYV	274	11	1215
HISYPPLHEW	298	10	1216
HISYPPLHEWV	298	11	1217
HMVKISGGPHI	289	11	1218
IMPKAGLLI	195	9	1219
IMPKAGLLII	195	10	1220
IMPKAGLLIIV	195	11	1221
KISGGPHI	292	8	1222
KISGGPHISY	292	10	1223
KIWEELSV	220	8	1224
KIWEELSVLEV	220	11	1225
KLLTQHFV	244	8	1226
KVAELVHF	112	8	1227
KVLHHMVKI	285	9	1228
LIIVLAII	202	8	1229
LLGDNQIM	189	8	1230
LLIIVLAI	201	8	1231
LLIIVLAII	201	9	1232
LLKYRAREPV	121	10	1233

Table XIV B

Mage 3 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
LLLKYRAREPV	120	11	1234
LLTQHFVQENY	245	11	1235
LMEVDPIGHLY	166	11	1236
LPTTMNYPLW	71	10	1237
LQLVFGIELM	158	10	1238
LVETSYVKV	278	9	1239
LVEVTLGEV	45	9	1240
LVFGIELM	160	8	1241
LVFGIELMEV	160	10	1242
LVHFLLLKY	116	9	1243
MLGSVVGNW	135	9	1244
MLGSVVGNWQY	135	11	1245
MPKAGLLI	196	8	1246
MPKAGLLII	196	9	1247
MPKAGLLIIV	196	10	1248
MVKISGGPHI	290	10	1249
NQEEEGPSTF	89	10	1250
NQIMPKAGLLI	193	11	1251
PIGHLYIF	171	8	1252
PQGASSLPTTM	65	11	1253
PVTKAEMLGSV	129	11	1254
QIMPKAGLLI	194	10	1255
QIMPKAGLLII	194	11	1256
QLVFGIELM	159	9	1257
QLVFGIELMEV	159	11	1258
QVPGSDPACY	260	10	1259
RQVPGSDPACY	259	11	1260
SLPTTMNY	70	8	1261
SLPTTMNYPLW	70	11	1262
SLQLVFGI	157	8	1263
SLQLVFGIELM	157	11	1264
SVVGNWQY	138	8	1265
SVVGNWQYF	138	9	1266
SVVGNWQYFF	138	10	1267
TLVEVTLGEV	44	10	1268
TMNYPLWSQSY	74	11	1269
TQHFVQENY	247	9	1270
VLHHMVKI	286	8	1271
VPGSDPACY	261	9	1272
VPGSDPACYEF	261	11	1273
VQENYLEY	251	8	1274
VQENYLEYRQV	251	11	1275
VVGNWQYF	139	8	1276
VVGNWQYFF	139	9	1277
VVGNWQYFFPV	139	11	1278
WQYFFPVI	143	8	1279

Table XIV B

Mage 3 B62 Supermotif Peptides

Sequence	Position	No. of Amino Acids	SEQ ID NO.
WQYFFPVIF	143	9	1280
YIFATCLGLSY	176	11	1281
YPLWSQSY	77	8	1282
YPPLHEWV	301	8	1283
YVKVLHHM	283	8	1284
YVKVLHHMV	283	9	1285
YVKVLHHMVKI	283	11	1286

Table XV A

Mage 2 A01 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASSFSTTINY	68	10	0.1700	1287
GASSFSTTINY	67	11	0.0047	1288
GGEPHISY	294	8	-0.0021	1289
IFSKASEY	150	8	0.0023	1290
LMQDLVQENY	246	10	0.0450	1291
MQDLVQENY	247	9	1.5000	1292
PGSDPACY	262	8	-0.0021	1293
PRALIETSY	275	9	-0.0006	1294
SFSTTINY	70	8	-0.0021	1295
SSFSTTINY	69	9	0.0430	1296
VQENYLEY	251	8	-0.0021	1297
VTCLGLSY	179	8		1298
VVEVVPISHLY	166	11	0.2000	1299

Table XV B

Mage 3 A01 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0101	SEQ ID NO.
ASSLPTTMNY	68	10	2.6000	1300
ATCLGLSY	179	8	0.1100	1301
EVDPIGHLY	168	9	18.0000	1302
GASSLPTTMNY	67	11	0.0390	1303
GSVVGNWQY	137	9	0.0500	1304
IFATCLGLSY	177	10	0.0020	1305
ISGGPHISY	293	9	0.0370	1306
KISGGPHISY	292	10	0.0011	1307
LGSVVGNWQY	136	10	0.0020	1308
LMEVDPIGHLY	166	11	7.5000	1309
LTQHFVQENY	246	10	0.2600	1310
PGSDPACY	262	8	-0.0021	1311
PRALVETSY	275	9	0.0011	1312
SSLPTTMNY	69	9	0.0550	1313
TMNYPLWSQSY	74	11	0.0830	1314
VQENYLEY	251	8	-0.0021	1315

Table XVI A

Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
AADSPSPPH	55	9	0.0003	1316
ACYEFLWGPR	267	10	0.0032	1317
ACYEFLWGPRA	267	11		1318
ADSPSPPH	56	8		1319
AIEGDCAPEEK	210	11	0.0009	1320
AIIAIEGDCA	207	10		1321
AISRKMVELVH	108	11		1322
ALGLVGAQA	22	9	0.0003	1323
ALGLVGAQAPA	22	11		1324
ALIETSYVK	277	9	0.0810	1325
ASEYLQLVF	154	9	0.0002	1326
ASSFSTTINY	68	10	0.0009	1327
ATEEQQTA	32	8		1328
DFFPVIFSK	145	9	0.0002	1329
DFFPVIFSKA	145	10		1330
DLESEFQA	100	8		1331
DLESEFQAA	100	9		1332
DLVQENYLEY	249	10		1333
DLVQENYLEYR	249	11	0.0047	1334
DSVFAHPR	236	8	-0.0004	1335
DSVFAHPRK	236	9	0.0021	1336
EALGLVGA	21	8		1337
EALGLVGAQA	21	10	0.0003	1338
EDSVFAHPR	235	9		1339
EDSVFAHPRK	235	10		1340
EFLWGPRA	270	8		1341
EFQAAISR	104	8		1342
EFQAAISRK	104	9	0.0002	1343
EGDCAPEEK	212	9	0.0002	1344
EGLEARGEA	14	9	0.0003	1345
EGREDSVF	232	8		1346
EGREDSVFA	232	9		1347
EGREDSVFAH	232	10		1348
ELSMLEVF	224	8		1349
ELSMLEVFEGR	224	11	0.0016	1350
ELVHFLLLK	115	9	0.0045	1351
ELVHFLLLKY	115	10	0.0066	1352
ELVHFLLLKYR	115	11	0.0011	1353
EMLESVLR	134	8	-0.0009	1354
ESEFQAAISR	102	10	0.0002	1355
ESEFQAAISRK	102	11	0.0010	1356
ESVLRNCQDF	137	10	0.0002	1357
ESVLRNCQDFF	137	11		1358
ETSYVKVLH	280	9		1359
ETSYVKVLHH	280	10		1360
EVFEGREDSVF	229	11		1361

Table XVI A

Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
EVTLGEVPA	47	9	0.0003	1362
EVTLGEVPAA	47	10	0.0003	1363
EVVEVVPISH	165	10	0.0002	1364
EVVPISHLY	168	9	0.0002	1365
FFPVIFSK	146	8		1366
FFPVIFSKA	146	9	0.0003	1367
FLLLKYRA	119	8		1368
FLLLKYRAR	119	9		1369
FSTTINYTLWR	71	11	0.0110	1370
GASSFSTTINY	67	11		1371
GDCAPEEK	213	8		1372
GDNQVMPK	191	8		1373
GGEPHISY	294	8		1374
GLEARGEA	15	8		1375
GLLGDNQVMPK	188	11	0.0780	1376
GLLIIVLA	200	8		1377
GLLIIVLAIIA	200	11		1378
GLVGAQAPA	24	9	0.0003	1379
GSDPACYEF	263	9		1380
GSSNQEEEGPR	86	11	-0.0002	1381
HCKPEEGLEA	9	10	0.0003	1382
HCKPEEGLEAR	9	11		1383
HFLLLKYR	118	8		1384
HFLLLKYRA	118	9	0.0016	1385
HFLLLKYRAR	118	10	0.0014	1386
HISYPPLH	298	8		1387
HISYPPLHER	298	10	0.0074	1388
HISYPPLHERA	298	11		1389
HSPQGASSF	63	9	0.0002	1390
HTLKIGGEPH	289	10		1391
IAIEGDCA	209	8		1392
IFSKASEY	150	8		1393
IGGEPHISY	293	9		1394
IIAIEGDCA	208	9		1395
IIVLAIIA	203	8		1396
ILVTCLGLSY	177	10	0.0036	1397
ISRKMVELVH	109	10	0.0002	1398
ISRKMVELVHF	109	11		1399
ISYPPLHER	299	9	0.0340	1400
ISYPPLHERA	299	10		1401
KAEMLESVLR	132	10	0.0002	1402
KASEYLQLVF	153	10	0.0002	1403
KIGGEPHISY	292	10		1404
KMVELVHF	112	8		1405
KTGLLIIVLA	198	10		1406
KVLHHTLK	285	8	0.0053	1407

Table XVI A

Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
LAIIAIEGDCA	206	11		1408
LGDNQVMPK	190	9	0.0002	1409
LGLVGAQA	23	8		1410
LGLVGAQAPA	23	10	0.0003	1411
LIETSYVK	278	8	-0.0004	1412
LIETSYVKVLH	278	11		1413
LIIVLAIIA	202	9		1414
LLGDNQVMPK	189	10	0.0093	1415
LLIIVLAIIA	201	10		1416
LLLKYRAR	120	8	-0.0009	1417
LLMQDLVQENY	245	11		1418
LMQDLVQENY	246	10		1419
LSMLEVFEGR	225	10	-0.0004	1420
LVEVTLGEVPA	45	11		1421
LVGAQAPA	25	8		1422
LVHFLLLK	116	8	0.0290	1423
LVHFLLLKY	116	9	0.0430	1424
LVHFLLLKYR	116	10	0.0260	1425
LVHFLLLKYRA	116	11		1426
LVQENYLEY	250	9		1427
LVQENYLEYR	250	10	0.0027	1428
LVTCLGLSY	178	9		1429
MFPDLESEF	97	9	0.0002	1430
MFPDLESEFQA	97	11		1431
MLEVFEGR	227	8	-0.0009	1432
MVELVHFLLLK	113	11	0.0200	1433
NCQDFFPVIF	142	10	0.0002	1434
PAADSPSPPH	54	10		1435
PACYEFLWGPR	266	11	-0.0009	1436
PATEEQQTA	31	9		1437
PDLESEFQA	99	9	0.0003	1438
PDLESEFQAA	99	10	0.0003	1439
PGSDPACY	262	8		1440
PGSDPACYEF	262	10		1441
PLEQRSQH	2	8		1442
PLEQRSQHCK	2	10	0.0003	1443
PLHERALR	303	8	-0.0009	1444
PSPPHSPQGA	59	10		1445
PVIFSKASEY	148	10	0.0160	1446
QAPATEEQQTA	29	11		1447
QDFFPVIF	144	8		1448
QDFFPVIFSK	144	10	0.0002	1449
QDFFPVIFSKA	144	11		1450
QDLVQENY	248	8		1451
QDLVQENYLEY	248	11		1452
QVPGSDPA	260	8		1453

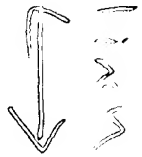

Table XVI A

Mage 2 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
QVPGSDPACY	260	10		1454
RALIETSY	276	8		1455
RALIETSYVK	276	10	0.0200	1456
RAREPVTK	125	8	-0.0009	1457
RAREPVTKA	125	9		1458
RGEALGLVGA	19	10	0.0003	1459
RMFPDLESEF	96	10	0.0002	1460
SDPACYEF	264	8		1461
SFSTTINY	70	8		1462
SMLEVFEGR	226	9	0.0020	1463
SSFSTTINY	69	9		1464
SSNQEEEGPR	87	10	0.0002	1465
STTINYTLWR	72	10	0.0014	1466
SVFAHPRK	237	8	0.1410	1467
SVLRNCQDF	138	9	0.0002	1468
SVLRNCQDFF	138	10	0.0002	1469
TGLLIIVLA	199	9		1470
TINYTLWR	74	8	0.0140	1471
TLGEVPAA	49	8		1472
TLKIGGEPH	290	9		1473
TSYVKVLH	281	8		1474
TSYVKVLHH	281	9	0.5900	1475
TTINYTLWR	73	9	0.0890	1476
VFEGREDSVF	230	10		1477
VFEGREDSVFA	230	11		1478
VIFSKASEY	149	9	0.0810	1479
VLRNCQDF	139	8		1480
VLRNCQDFF	139	9	0.0002	1481
VTCLGLSY	179	8		1482
VTLGEVPA	48	8		1483
VTLGEVPAA	48	9	0.0003	1484
VVEVVPISH	166	9	0.0007	1485
VVEVVPISHLY	166	11		1486
VVPISHLY	169	8		1487
WGPRALIETSY	273	11		1488
YILVTCLGLSY	176	11		1489
YVKVLHHTLK	283	10	0.0033	1490

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
AALSRKVA	107	8		1491
ACYEFLWGPR	267	10	0.0032	1492
ACYEFLWGPRA	267	11		1493
AGLLIIVLA	199	9	0.0006	1494
AIIAREGDCA	207	10		1495
ALGLVGAQA	22	9	0.0003	1496
ALGLVGAQAPA	22	11		1497
ALSRKVAELVH	108	11		1498
ALVETSYVK	277	9	0.0270	1499
ASSLPTTMNY	68	10	0.0009	1500
ASSSLQLVF	154	9	0.0011	1501
ATCLGLSY	179	8		1502
ATEEQEAA	32	8		1503
DLESEFQA	100	8		1504
DLESEFQAA	100	9		1505
DSILGDPK	236	8	-0.0004	1506
DSILGDPKK	236	9	-0.0003	1507
EALGLVGA	21	8		1508
EALGLVGAQA	21	10	0.0003	1509
EDSILGDPK	235	9	0.0003	1510
EDSILGDPKK	235	10	0.0003	1511
EFLWGPRA	270	8		1512
EFQAALSR	104	8		1513
EFQAALSRK	104	9	0.0002	1514
EFQAALSRKVA	104	11		1515
EGDCAPEEK	212	9	0.0002	1516
EGLEARGEA	14	9	0.0003	1517
ELMEVDPIGH	165	10	0.0003	1518
ELSVLEVF	224	8		1519
ELSVLEVFEGR	224	11	-0.0009	1520
ELVHFLLLK	115	9	0.0045	1521
ELVHFLLLKY	115	10	0.0066	1522
ELVHFLLLKYR	115	11	0.0011	1523
ESEFQAALSR	102	10	0.0002	1524
ESEFQAALSRK	102	11	0.0002	1525
ETSYVKVLH	280	9		1526
ETSYVKVLHH	280	10		1527
EVDPIGHLY	168	9	0.0002	1528
EVDPIGHLYIF	168	11		1529
EVTLGEVPA	47	9	0.0003	1530
EVTLGEVPAA	47	10	0.0003	1531
FATCLGLSY	178	9	0.0003	1532
FFPVIFSK	146	8		1533
FFPVIFSKA	146	9	0.0003	1534
FLLLKYRA	119	8		1535
FLLLKYRAR	119	9		1536

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
FVQENYLEY	250	9		1537
FVQENYLEYR	250	10	0.0009	1538
GASSLPTTMNY	67	11		1539
GDCAPEEK	213	8		1540
GDNQIMPK	191	8		1541
GDNQIMPKA	191	9	0.0003	1542
GDPKKLLTQH	240	10	0.0003	1543
GDPKKLLTQHF	240	11		1544
GGPHISYPPLH	295	11		1545
GLEARGEA	15	8		1546
GLLGDNQIMPK	188	11	0.1300	1547
GLLIIVLA	200	8		1548
GLLIIVLAIIA	200	11		1549
GLVGAQAPA	24	9	0.0003	1550
GSDPACYEF	263	9		1551
GSVVGNWQY	137	9		1552
GSVVGNWQYF	137	10	0.0020	1553
GSVVGNWQYFF	137	11		1554
HCKPEEGLEA	9	10	0.0003	1555
HCKPEEGLEAR	9	11		1556
HFLLLKYR	118	8		1557
HFLLLKYRA	118	9	0.0016	1558
HFLLLKYRAR	118	10	0.0014	1559
HFVQENYLEY	249	10		1560
HFVQENYLEYR	249	11		1561
HISYPPLH	298	8		1562
HMVKISGGPH	289	10		1563
IAREGDCA	209	8		1564
IFATCLGLSY	177	10	0.0005	1565
IGHLYIFA	172	8		1566
IIAREGDCA	208	9		1567
IIVLAIIA	203	8		1568
IIVLAIIAR	203	9	0.0069	1569
ISGGPHISY	293	9	0.0003	1570
IVLAIIAR	204	8	0.0053	1571
KAGLLIIVLA	198	10		1572
KASSSLQLVF	153	10	0.0003	1573
KISGGPHISY	292	10		1574
KVAELVHF	112	8		1575
KVLHHMVK	285	8	0.0580	1576
LAIIAREGDCA	206	11		1577
LGDNQIMPK	190	9		1578
LGDNQIMPKA	190	10	0.0003	1579
LGDPKKLLTQH	239	11		1580
LGLVGAQA	23	8		1581
LGLVGAQAPA	23	10	0.0003	1582

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
LGSVVGNWQY	136	10	0.0003	1583
LGSVVGNWQYF	136	11		1584
LIIVLAIIA	202	9		1585
LIIVLAIIAR	202	10	0.0280	1586
LLGDNQIMPK	189	10	0.0200	1587
LLGDNQIMPKA	189	11		1588
LLIIVLAIIA	201	10		1589
LLIIVLAIIAR	201	11	0.0021	1590
LLLKYRAR	120	8	-0.0009	1591
LLTQHFVQENY	245	11		1592
LMEVDPIGH	166	9	0.0002	1593
LMEVDPIGHLY	166	11		1594
LSRKVAELVH	109	10	0.0002	1595
LSRKVAELVHF	109	11		1596
LSVLEVFEGR	225	10	-0.0006	1597
LTQHFVQENY	246	10	0.0003	1598
LVETSYVK	278	8	-0.0004	1599
LVETSYVKVLH	278	11		1600
LVEVTLGEVPA	45	11		1601
LVGAQAPA	25	8		1602
LVHFLLLK	116	8	0.0290	1603
LVHFLLLKY	116	9	0.0430	1604
LVHFLLLKYR	116	10	0.0260	1605
LVHFLLLKYRA	116	11		1606
MLGSVVGNWQY	135	11		1607
MVKISGGPH	290	9	0.0003	1608
PACYEFLWGPR	266	11	-0.0009	1609
PATEEQEA	31	8		1610
PATEEQEAA	31	9	0.0003	1611
PDLESEFQA	99	9	0.0003	1612
PDLESEFQAA	99	10	0.0003	1613
PDPPQSPQGA	59	10	0.0003	1614
PGSDPACY	262	8		1615
PGSDPACYEF	262	10		1616
PIGHLYIF	171	8		1617
PIGHLYIFA	171	9		1618
PLEQRSQH	2	8		1619
PLEQRSQHCK	2	10	0.0003	1620
PLHEWVLR	303	8	-0.0009	1621
PSTFPDLESEF	95	11		1622
QAALSRKVA	106	9		1623
QAPATEEQEA	29	10	0.0003	1624
QAPATEEQEAA	29	11		1625
QVPGSDPA	260	8		1626
QVPGSDPACY	260	10		1627
RALVETSY	276	8		1628

Table XVI B

Mage 3 A03 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*0301	SEQ ID NO.
RALVETSYVK	276	10	0.0190	1629
RAREPVTK	125	8	-0.0009	1630
RAREPVTKA	125	9		1631
RGEALGLVGA	19	10	0.0003	1632
SDPACYEF	264	8		1633
SGGPHISY	294	8		1634
SILGDPKK	237	8	-0.0009	1635
SLPTTMNY	70	8		1636
SSLPTTMNY	69	9		1637
SSSLQLVF	155	8		1638
STFPDLESEF	96	10	0.0002	1639
SVLEVFEGR	226	9	0.0003	1640
SVVGNWQY	138	8		1641
SVVGNWQYF	138	9	0.0002	1642
SVVGNWQYFF	138	10	0.0085	1643
TFPDLESEF	97	9	0.0002	1644
TFPDLESEFQA	97	11		1645
TLGEVPAA	49	8		1646
TMNYPLWSQSY	74	11		1647
TSYVKVLH	281	8		1648
TSYVKVLHH	281	9	0.5900	1649
VAELVHFLLLK	113	11	-0.0002	1650
VDPIGHLY	169	8		1651
VDPIGHLYIF	169	10	0.0003	1652
VDPIGHLYIFA	169	11		1653
VGNWQYFF	140	8		1654
VLEVFEGR	227	8	0.0016	1655
VTLGEVPA	48	8		1656
VTLGEVPAA	48	9	0.0003	1657
VVGNWQYF	139	8		1658
VVGNWQYFF	139	9	0.0022	1659
WGPRALVETSY	273	11		1660
YFFPVIFSK	145	9	0.0020	1661
YFFPVIFSKA	145	10	0.0003	1662
YIFATCLGLSY	176	11		1663
YVKVLHHMVK	283	10	0.0020	1664

Table XVII A

Mage 2 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
AADSPSPPH	55	9	0.0009	1665
ACYEFLWGPR	267	10	0.0035	1666
ADSPSPPH	56	8		1667
AIEGDCAPEEK	210	11	0.0007	1668
AISRKMVELVH	108	11		1669
ALIETSYVK	277	9	0.1900	1670
ASSFSTTINY	68	10	0.0260	1671
DFFPVIFSK	145	9	0.0022	1672
DLVQENYLEY	249	10		1673
DLVQENYLEYR	249	11	0.0018	1674
DSVFAHPR	236	8	0.0005	1675
DSVFAHPRK	236	9	0.0025	1676
EDSVFAHPR	235	9		1677
EDSVFAHPRK	235	10		1678
EFQAAISR	104	8		1679
EFQAAISRK	104	9	0.0002	1680
EGDCAPEEK	212	9	0.0001	1681
EGREDSVFAH	232	10		1682
ELSMLEVFEGR	224	11	0.0008	1683
ELVHFLLLK	115	9	0.0011	1684
ELVHFLLLKY	115	10	0.0003	1685
ELVHFLLLKYR	115	11	0.0031	1686
EMLESVLR	134	8	-0.0003	1687
ESEFQAAISR	102	10	0.0002	1688
ESEFQAAISRK	102	11	0.0004	1689
ETSYVKVLH	280	9		1690
ETSYVKVLHH	280	10		1691
EVVEVVPISH	165	10	0.0002	1692
EVVPISHLY	168	9	0.0002	1693
FFPVIFSK	146	8		1694
FLLLKYRAR	119	9		1695
FSTTINYTLWR	71	11	0.0170	1696
GASSFSTTINY	67	11		1697
GDCAPEEK	213	8		1698
GDNQVMPK	191	8		1699
GGEPHISY	294	8		1700
GLLGDNQVMPK	188	11	0.0047	1701
GSSNQEEEGPR	86	11	-0.0002	1702
HCKPEEGLEAR	9	11		1703
HFLLLKYR	118	8		1704
HFLLLKYRAR	118	10	0.0002	1705
HISYPPLH	298	8		1706
HISYPPLHER	298	10	0.0018	1707
HTLKIGGEPH	289	10		1708
IFSKASEY	150	8		1709
IGGEPHISY	293	9		1710

Table XVII A

Mage 2 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
ILVTCLGLSY	177	10	0.0002	1711
ISRKMVELVH	109	10	0.0002	1712
ISYPPLHER	299	9	0.0280	1713
KAEMLESVLR	132	10	0.0009	1714
KIGGEPHISY	292	10		1715
KVLHHTLK	285	8	0.0100	1716
LGDNQVMPK	190	9	0.0061	1717
LIETSYVK	278	8	0.0027	1718
LIETSYVKVLH	278	11		1719
LLGDNQVMPK	189	10	0.0014	1720
LLLKYRAR	120	8	-0.0004	1721
LLMQDLVQENY	245	11		1722
LMQDLVQENY	246	10		1723
LSMLEVFEGR	225	10	0.0001	1724
LVHFLLLK	116	8	0.1500	1725
LVHFLLLKY	116	9	0.0100	1726
LVHFLLLKYR	116	10	0.0022	1727
LVQENYLEY	250	9		1728
LVQENYLEYR	250	10	0.0089	1729
LVTCLGLSY	178	9		1730
MLEVFEGR	227	8	-0.0004	1731
MVELVHFLLLK	113	11	0.0120	1732
PAADSPSPPH	54	10		1733
PACYEFLWGPR	266	11	-0.0002	1734
PGSDPACY	262	8		1735
PLEQRSQH	2	8		1736
PLEQRSQHCK	2	10	0.0002	1737
PLHERALR	303	8	-0.0004	1738
PVIFSKASEY	148	10	0.0033	1739
QDFFPVIFSK	144	10	0.0083	1740
QDLVQENY	248	8		1741
QDLVQENYLEY	248	11		1742
QVPGSDPACY	260	10		1743
RALIETSY	276	8		1744
RALIETSYVK	276	10	0.0750	1745
RAREPVTK	125	8	-0.0003	1746
SFSTTINY	70	8		1747
SMLEVFEGR	226	9	0.0220	1748
SNQEEEGPR	88	9	0.0001	1749
SSFSTTINY	69	9		1750
SSNQEEEGPR	87	10	0.0002	1751
STTINYTLWR	72	10	0.0910	1752
SVFAHPRK	237	8	0.0810	1753
TINYTLWR	74	8	0.0550	1754
TLKIGGEPH	290	9		1755
TSYVKVLH	281	8		1756

Table XVII A

Mage 2 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
TSYVKVLHH	281	9	0.0066	1757
TTINYTLWR	73	9	1.1000	1758
VIFSKASEY	149	9	0.0330	1759
VTCLGLSY	179	8		1760
VVEVVPISH	166	9	0.0100	1761
VVEVVPISHLY	166	11		1762
VVPISHLY	169	8		1763
WGPRALIETSY	273	11		1764
YILVTCLGLSY	176	11		1765
YVKVLHHTLK	283	10	0.0160	1766

Table XVII B

Mage 3 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
ACYEFLWGPR	267	10	0.0035	1767
ALSRKVAELVH	108	11		1768
ALVETSYVK	277	9	0.1700	1769
ASSLPTTMNY	68	10	0.0330	1770
ATCLGLSY	179	8		1771
DSILGDPK	236	8	-0.0003	1772
DSILGDPKK	236	9	-0.0002	1773
EDSILGDPK	235	9	0.0002	1774
EDSILGDPKK	235	10	0.0002	1775
EFQAALSR	104	8		1776
EFQAALSRK	104	9	0.0001	1777
EGDCAPEEK	212	9	0.0001	1778
ELMEVDPIGH	165	10	0.0002	1779
ELSVLEVFEGR	224	11	0.0023	1780
ELVHFLLLK	115	9	0.0011	1781
ELVHFLLLKY	115	10	0.0003	1782
ELVHFLLLKYR	115	11	0.0031	1783
ESEFQAALSR	102	10	0.0002	1784
ESEFQAALSRK	102	11	0.0004	1785
ETSYVKVLH	280	9		1786
ETSYVKVLHH	280	10		1787
EVDPIGHLY	168	9	0.0009	1788
FATCLGLSY	178	9	0.0004	1789
FFPVIFSK	146	8		1790
FLLLKYRAR	119	9		1791
FVQENYLEY	250	9		1792
FVQENYLEYR	250	10	0.0012	1793
GASSLPTTMNY	67	11		1794
GDCAPEEK	213	8		1795
GDNQIMPK	191	8		1796
GDPKKLLTQH	240	10	0.0002	1797
GGPHISYPPLH	295	11		1798
GLLGDNQIMPK	188	11	0.0570	1799
GSVVGNWQY	137	9		1800
HCKPEEGLEAR	9	11		1801
HFLLLKYR	118	8		1802
HFLLLKYRAR	118	10	0.0002	1803
HFVQENYLEY	249	10		1804
HFVQENYLEYR	249	11		1805
HISYPPLH	298	8		1806
HMVKISGGPH	289	10		1807
IFATCLGLSY	177	10	0.0004	1808
IIVLAIIAR	203	9	0.0011	1809
ISGGPHISY	293	9	0.0002	1810
IVLAIIAR	204	8	0.0037	1811
KISGGPHISY	292	10		1812
KVLHHMVK	285	8	0.0190	1813

Table XVII B

Mage 3 A11 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*1101	SEQ ID NO.
LGDNQIMPK	190	9		1814
LGDPKKLLTQH	239	11		1815
LGSVVGNWQY	136	10	0.0012	1816
LIIVLAIIAR	202	10	0.0021	1817
LLGDNQIMPK	189	10	0.0110	1818
LLIIVLAIIAR	201	11	0.0056	1819
LLLKYRAR	120	8	-0.0004	1820
LLTQHFVQENY	245	11		1821
LMEVDPIGH	166	9	0.0001	1822
LMEVDPIGHLY	166	11		1823
LSRKVAELVH	109	10	0.0002	1824
LSVLEVFEGR	225	10	0.0030	1825
LTQHFVQENY	246	10	0.0002	1826
LVETSYVK	278	8	0.0014	1827
LVETSYVKVLH	278	11		1828
LVHFLLLK	116	8	0.1500	1829
LVHFLLLKY	116	9	0.0100	1830
LVHFLLLKYR	116	10	0.0022	1831
MLGSVVGNWQY	135	11		1832
MNYPLWSQSY	75	10	0.0002	1833
MVKISGGPH	290	9	0.0002	1834
PACYEFLWGPR	266	11	-0.0002	1835
PGSDPACY	262	8		1836
PLEQRSQH	2	8		1837
PLEQRSQHCK	2	10	0.0002	1838
PLHEWVLR	303	8	-0.0003	1839
QVPGSDPACY	260	10		1840
RALVETSY	276	8		1841
RALVETSYVK	276	10	0.1100	1842
RAREPVTK	125	8	-0.0003	1843
SGGPHISY	294	8		1844
SILGDPKK	237	8	0.0012	1845
SLPTTMNY	70	8		1846
SSLPTTMNY	69	9		1847
SVLEVFEGR	226	9	0.1400	1848
SVVGNWQY	138	8		1849
TMNYPLWSQSY	74	11		1850
TSYVKVLH	281	8		1851
TSYVKVLHH	281	9	0.0066	1852
VAELVHFLLLK	113	11	0.0011	1853
VDPIGHLY	169	8		1854
VLEVFEGR	227	8	0.0005	1855
WGPRALVETSY	273	11		1856
YFFPVIFSK	145	9	0.0270	1857
YIFATCLGLSY	176	11		1858
YVKVLHHMVK	283	10	0.0061	1859

Table XVIII A

Mage 2 A24 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
CYEFLWGPRAL	268	11	0.0004	1860
EFLWGPRAL	270	9	0.0006	1861
EFLWGPRALI	270	10	0.0097	1862
EYLQLVFGI	156	9	3.5000	1863
IFSKASEYL	150	9	0.0230	1864
IFSKASEYLQL	150	11	0.0950	1865
IWEELSML	221	8	0.0007	1866
IWEELSMLEVF	221	11	0.0170	1867
KMVELVHF	112	8	0.0005	1868
KMVELVHFL	112	9		1869
KMVELVHFLL	112	10		1870
KMVELVHFLLL	112	11		1871
LMQDLVQENYL	246	11		1872
LWGPRALI	272	8	0.1200	1873
LYILVTCL	175	8	0.0086	1874
LYILVTCLGL	175	10	0.0140	1875
MFPDLESEF	97	9	0.0140	1876
RMFPDLESEF	96	10	0.0016	1877
SFSTTINYTL	70	10	0.0150	1878
SFSTTINYTLW	70	11	0.0280	1879
SYPPLHERAL	300	10	0.0003	1880
SYVKVLHHTL	282	10	0.1600	1881
VFAHPRKL	238	8	0.0005	1882
VFAHPRKLL	238	9	0.0006	1883
VFEGREDSVF	230	10	0.0004	1884
VMPKTGLL	195	8	-0.0004	1885
VMPKTGLLI	195	9	0.2300	1886
VMPKTGLLII	195	10	0.0580	1887

Table XVIII B

Mage 3 A24 Motif Peptides with Binding Data

Sequence	Position	No. of Amino Acids	A*2401	SEQ ID NO.
CYEFLWGPRAL	268	11	0.0004	1888
EFLWGPRAL	270	9	0.0006	1889
EMLGSVVGNW	134	10	0.0017	1890
HFVQENYL	249	8	-0.0004	1891
HMVKISGGPHI	289	11		1892
IFATCLGL	177	8	0.0120	1893
IFSKASSSL	150	9	0.0160	1894
IFSKASSSLQL	150	11	0.0910	1895
IMPKAGLL	195	8		1896
IMPKAGLLI	195	9	0.4200	1897
IMPKAGLLII	195	10	0.0500	1898
IWEELSVL	221	8	-0.0004	1899
IWEELSVLEVF	221	11	0.0260	1900
LMEVDPIGHL	166	10		1901
LYIFATCL	175	8	0.0140	1902
LYIFATCLGL	175	10	0.0480	1903
NWQYFFPVI	142	9	0.5300	1904
NWQYFFPVIF	142	10	0.0170	1905
QYFFPVIF	144	8	0.1200	1906
SYDGLLGDNQI	185	11	0.0026	1907
SYPPLHEW	300	8	0.0420	1908
SYPPLHEWVL	300	10	0.5900	1909
TFPDLESEF	97	9	0.0049	1910
VFEGREDSI	230	9	-0.0004	1911
VFEGREDSIL	230	10	-0.0005	1912

Table XIX A **Mage 2 DR Super Motif Peptides with Binding Data**

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LVGAQAPAT	2044	ALGLVGAQAPATEEQ	1913	24	0.0330				-0.0032			
LSYDGLLGD	2045	CLGLSYDGLLGDNQV	1914	183				0.1400				
LGDNQVMPK	2046	DGLLGDNQVMPKTGL	1915	189	-0.0005				-0.0032			
IWEELSMLE	2047	EEKIWEELSMLEVFE	1916	220				0.0130				
WGPRALIET	2048	EFLWGPRALIETSYV	1917	272								
WEELSMLEV	2049	EKIWEELSMLEVFEG	1918	221								
LEYRQVPGS	2050	ENYLEYRQVPGSDPA	1919	255								
ISYPPLHER	2051	EPHISYPPLHERALR	1920	298	-0.0003				-0.0032			
FQAAISRKM	2052	ESEFQAAISRKMVEL	1921	104	1.2000	0.0620	1.0000	0.0113	0.1600		0.0270	
LGEVPAADS	2053	EVTLGEVPAADSPSP	1922	49								
VIFSKASEY	2054	FFPVIFSKASEYLQL	1923	148								
IFSKASEYL	2055	FPVIFSKASEYLQLV	1924	149								
LGLVGAQAP	2056	GEALGLVGAQAPATE	1925	22								
VVEVVPISH	2057	GIEVVEVVPISHLYI	1926	165	0.0084	0.0046	0.0009	0.0036	0.0070		-0.0005	
IIVLAIIAI	2058	GLLIIVLAIIAIEGD	1927	202	0.0100				-0.0032			
LLKYRAREP	2059	HFLLLKYRAREPVTK	1928	120								
ILVTCLGLS	2060	HLYILVTCLGLSYDG	1929	176								
VEVVPISHL	2061	IEVVEVVPISHLYIL	1930	166								
IEGDCAPEE	2062	IIAIEGDCAPEEKIW	1931	210				0.0660				
LAIIAIEGD	2063	IIVLAIIAIEGDCAP	1932	205								
LYILVTCLG	2064	ISHLYILVTCLGLSY	1933	174								
MLESVLRNC	2065	KAEMLESVLRNCQDF	1934	134								
LLIIVLAII	2066	KTGLLIIVLAIIAIE	1935	200	0.0120	0.0037	-0.0022	0.0025	0.0370		-0.0005	
VPAADSPSP	2067	LGEVPAADSPSPPHS	1936	52	-0.0005				-0.0032			
VGAQAPATE	2068	LGLVGAQAPATEEQQ	1937	25								
VLAIIAIEG	2069	LIIVLAIIAIEGDCA	1938	204	0.0120				0.0051			
IVLAIIAIE	2070	LLIIVLAIIAIEGDC	1939	203	0.0086				0.0120			
YRAREPVTK	2071	LLKYRAREPVTKAEM	1940	123								
VFGIEVVEV	2072	LQLVFGIEVVEVVPI	1941	160								
VTLGEVPAA	2073	LVEVTLGEVPAADSP	1942	47								
LVHFLLLKY	2074	MVELVHFLLLKYRAR	1943	115								
MPKTGLLII	2075	NQVMPKTGLLIIVLA	1944	195	0.0019				-0.0032			
LLMQDLVQE	2076	PRKLLMQDLVQENYL	1945	244								
FPDLESEFQ	2077	PRMFPDLESEFQAAI	1946	97								
ISRKMVELV	2078	QAAISRKMVELVHFL	1947	108								
FPVIFSKAS	2079	QDFFPVIFSKASEYL	1948	146								
VQENYLEYR	2080	QDLVQENYLEYRQVP	1949	250								
FGIEVVEVV	2081	QLVFGIEVVEVVPIS	1950	161				0.0072				
IETSYVKVL	2082	RALIETSYVKVLHHT	1951	278								
VTKAEMLES	2083	REPVTKAEMLESVLR	1952	129								
LMQDLVQEN	2084	RKLLMQDLVQENYLE	1953	245				0.1500				
YILVTCLGL	2085	SHLYILVTCLGLSYD	1954	175								
LVEVTLGEV	2086	SSTLVEVTLGEVPAA	1955	44								
LIIVLAIIA	2087	TGLLIIVLAIIAIEG	1956	201	0.0008				-0.0032			
VHFLLLKYR	2088	VELVHFLLLKYRARE	1957	116								
VPISHLYIL	2089	VEVVPISHLYILVTC	1958	169								
IEVVEVVPI	2090	VFGIEVVEVVPISHL	1959	163								
ISHLYILVT	2091	VVPISHLYILVTCLG	1960	171								
LSMLEVFEG	2092	WEELSMLEVFEGRED	1961	224								
LWGPRALIE	2093	YEFLWGPRALIETSY	1962	271								
VTCLGLSYD	2094	YILVTCLGLSYDGLL	1963	178								
LHERALREG	2095	YPPLHERALREGEE-	1964	303								

Table XIX A **Mage 2 DR Super Motif Peptides with Binding Data**

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LVGAQAPAT	2044	ALGLVGAQAPATEEQ	1913		-0.0011			
LSYDGLLGD	2045	CLGLSYDGLLGDNQV	1914					
LGDNQVMPK	2046	DGLLGDNQVMPKTGL	1915		-0.0011			
IWEELSMLE	2047	EEKIWEELSMLEVFE	1916					
WGPRALIET	2048	EFLWGPRALIETSYV	1917					
WEELSMLEV	2049	EKIWEELSMLEVFEG	1918					
LEYRQVPGS	2050	ENYLEYRQVPGSDPA	1919					
ISYPPLHER	2051	EPHISYPPLHERALR	1920		-0.0011			
FQAAISRKM	2052	ESEFQAAISRKMVEL	1921	0.0067	0.5100	0.0310		
LGEVPAADS	2053	EVTLGEVPAADSPSP	1922					
VIFSKASEY	2054	FFPVIFSKASEYLQL	1923					
IFSKASEYL	2055	FPVIFSKASEYLQLV	1924					
LGLVGAQAP	2056	GEALGLVGAQAPATE	1925					
VVEVVPISH	2057	GIEVVEVVPISHLYI	1926	0.0710	0.0900	0.0089		
IIVLAIIAI	2058	GLLIIVLAIIAIEGD	1927		-0.0011			
LLKYRAREP	2059	HFLLLKYRAREPVTK	1928					
ILVTCLGLS	2060	HLYILVTCLGLSYDG	1929					
VEVVPISHL	2061	IEVVEVVPISHLYIL	1930					
IEGDCAPEE	2062	IIAIEGDCAPEEKIW	1931					
LAIIAIEGD	2063	IIVLAIIAIEGDCAP	1932					
LYILVTCLG	2064	ISHLYILVTCLGLSY	1933					
MLESVLRNC	2065	KAEMLESVLRNCQDF	1934					
LLIIVLAII	2066	KTGLLIIVLAIIAIE	1935	0.0015	0.0290	-0.0004		
VPAADSPSP	2067	LGEVPAADSPSPPHS	1936		-0.0011			
VGAQAPATE	2068	LGLVGAQAPATEEQQ	1937					
VLAIIAIEG	2069	LIIVLAIIAIEGDCA	1938		0.0120			
IVLAIIAIE	2070	LLIIVLAIIAIEGDC	1939		0.0130			
YRAREPVTK	2071	LLKYRAREPVTKAEM	1940					
VFGIEVVEV	2072	LQLVFGIEVVEVVPI	1941					
VTLGEVPAA	2073	LVEVTLGEVPAADSP	1942					
LVHFLLLKY	2074	MVELVHFLLLKYRAR	1943					
MPKTGLLII	2075	NQVMPKTGLLIIVLA	1944		-0.0011			
LLMQDLVQE	2076	PRKLLMQDLVQENYL	1945					
FPDLESEFQ	2077	PRMFPDLESEFQAAI	1946					
ISRKMVELV	2078	QAAISRKMVELVHFL	1947					
FPVIFSKAS	2079	QDFFPVIFSKASEYL	1948					
VQENYLEYR	2080	QDLVQENYLEYRQVP	1949					
FGIEVVEVV	2081	QLVFGIEVVEVVPIS	1950					
IETSYVKVL	2082	RALIETSYVKVLHHT	1951					
VTKAEMLES	2083	REPVTKAEMLESVLR	1952					
LMQDLVQEN	2084	RKLLMQDLVQENYLE	1953					
YILVTCLGL	2085	SHLYILVTCLGLSYD	1954					
LVEVTLGEV	2086	SSTLVEVTLGEVPAA	1955					
LIIVLAIIA	2087	TGLLIIVLAIIAIEG	1956		-0.0011			
VHFLLLKYR	2088	VELVHFLLLKYRARE	1957					
VPISHLYIL	2089	VEVVPISHLYILVTC	1958					
IEVVEVVPI	2090	VFGIEVVEVVPISHL	1959					
ISHLYILVT	2091	VVPISHLYILVTCLG	1960					
LSMLEVFEG	2092	WEELSMLEVFEGRED	1961					
LWGPRALIE	2093	YEFLWGPRALIETSY	1962					
VTCLGLSYD	2094	YILVTCLGLSYDGLL	1963					
LHERALREG	2095	YPPLHERALREGEE-	1964					

Table XIX A **Mage 2 DR Super Motif Peptides with Binding Data**

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VPGSDPACY	2096	YRQVPGSDPACYEFL	1965	260								
VLHHTLKIG	2097	YVKVLHHTLKIGGEP	1966	285								

Table XIX A : Mage 2 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VPGSDPACY	2096	YRQVPGSDPACYEFL	1965					
VLHHTLKIG	2097	YVKVLHHTLKIGGEP	1966					

Table XIX B **Mage 3 DR Super Motif Peptides with Binding Data**

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VHFLLLKYR	2098	AELVHFLLLKYRARE	1967	116								
LIIVLAIIA	2099	AGLLIIVLAIIAREG	1968	201	0.0045				-0.0008			
LVGAQAPAT	2100	ALGLVGAQAPATEEQ	1969	24	0.0330				-0.0032			
LSYDGLLGD	2101	CLGLSYDGLLGDNQI	1970	183				-0.0025				
LGDNQIMPK	2102	DGLLGDNQIMPKAGL	1971	189	-0.0003				-0.0032			
IWEELSVLE	2103	EEKIWEELSVLEVFE	1972	220				0.0058				
WGPRALVET	2104	EFLWGPRALVETSYV	1973	272								
WEELSVLEV	2105	EKIWEELSVLEVFEG	1974	221								
LEYRQVPGS	2106	ENYLEYRQVPGSDPA	1975	255								
FQAALSRKV	2107	ESEFQAALSRKVAEL	1976	104	1.9000	0.3100	1.1000	0.0059	0.0590		0.0310	
LGEVPAAES	2108	EVTLGEVPAAESPDP	1977	49								
VIFSKASSS	2109	FFPVIFSKASSSLQL	1978	148								
IFSKASSSL	2110	FPVIFSKASSSLQLV	1979	149								
LGLVGAQAP	2111	GEALGLVGAQAPATE	1980	22								
YIFATCLGL	2112	GHLYIFATCLGLSYD	1981	175	0.0110				0.0110			
LMEVDPIGH	2113	GIELMEVDPIGHLYI	1982	165								
IIVLAIIAR	2114	GLLIIVLAIIAREGD	1983	202								
ISYPPLHEW	2115	GPHISYPPLHEWVLR	1984	298	0.0022				-0.0027			
LLKYRAREP	2116	HFLLLKYRAREPVTK	1985	120								
IFATCLGLS	2117	HLYIFATCLGLSYDG	1986	176								
MEVDPIGHL	2118	IELMEVDPIGHLYIF	1987	166	0.0003	0.0057	-0.0010	1.8000	-0.0055		-0.0008	
LYIFATCLG	2119	IGHLYIFATCLGLSY	1988	174								
MLGSVVGNW	2120	KAEMLGSVVGNWQYF	1989	134								
LLIIVLAII	2121	KAGLLIIVLAIIARE	1990	200	0.0043				-0.0008			
LTQHFVQEN	2122	KKLLTQHFVQENYLE	1991	245								
VPAAESPDP	2123	LGEVPAAESPDPPQS	1992	52								
VGAQAPATE	2124	LGLVGAQAPATEEQE	1993	25								
VLAIIAREG	2125	LIIVLAIIAREGDCA	1994	204								
IVLAIIARE	2126	LLIIVLAIIAREGDC	1995	203	0.0026				-0.0008			
YRAREPVTK	2127	LLKYRAREPVTKAEM	1996	123								
VFGIELMEV	2128	LQLVFGIELMEVDPI	1997	160	0.0250	0.0020	0.0013	0.0021	-0.0032		-0.0005	
VTLGEVPAA	2129	LVEVTLGEVPAAESP	1998	47								
MPKAGLLII	2130	NQIMPKAGLLIIVLA	1999	195	0.0440				-0.0032			
YFFPVIFSK	2131	NWQYFFPVIFSKASS	2000	144	0.1100	0.0030	0.0300	0.0006	0.1100		0.0650	
FPDLESEFQ	2132	PSTFPDLESEFQAAL	2001	97								
FSKASSSLQ	2133	PVIFSKASSSLQLVF	2002	150	0.0510	0.0170	-0.0007	0.0006	0.0240		-0.0005	
LSRKVAELV	2134	QAALSRKVAELVHFL	2003	108								
VQENYLEYR	2135	QHFVQENYLEYRQVP	2004	250								
FGIELMEVD	2136	QLVFGIELMEVDPIG	2005	161				0.0150				
FPVIFSKAS	2137	QYFFPVIFSKASSSL	2006	146								
VETSYVKVL	2138	RALVETSYVKVLHHM	2007	278								
VTKAEMLGS	2139	REPVTKAEMLGSVVG	2008	129								
LVEVTLGEV	2140	SSTLVEVTLGEVPAA	2009	44								
LVHFLLLKY	2141	VAELVHFLLLKYRAR	2010	115								
IGHLYIFAT	2142	VDPIGHLYIFATCLG	2011	171								
IELMEVDPI	2143	VFGIELMEVDPIGHL	2012	163								
WQYFFPVIF	2144	VGNWQYFFPVIFSKA	2013	142								
LSVLEVFEG	2145	WEELSVLEVFEGRED	2014	224								
LWGPRALVE	2146	YEFLWGPRALVETSY	2015	271								
LHEWVLREG	2147	YPPLHEWVLREGEE-	2016	303								
VPGSDPACY	2148	YRQVPGSDPACYEFL	2017	260								
VLHHMVKIS	2149	YVKVLHHMVKISGGP	2018	285								

Table XIX B **Mage 3 DR Super Motif Peptides with Binding Data**

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VHFLLLKYR	2098	AELVHFLLLKYRARE	1967					
LIIVLAIIA	2099	AGLLIIVLAIIAREG	1968		-0.0026			
LVGAQAPAT	2100	ALGLVGAQAPATEEQ	1969		-0.0011			
LSYDGLLGD	2101	CLGLSYDGLLGDNQI	1970					
LGDNQIMPK	2102	DGLLGDNQIMPKAGL	1971		-0.0011			
IWEELSVLE	2103	EEKIWEELSVLEVFE	1972					
WGPRALVET	2104	EFLWGPRALVETSYV	1973					
WEELSVLEV	2105	EKIWEELSVLEVFEG	1974					
LEYRQVPGS	2106	ENYLEYRQVPGSDPA	1975					
FQAALSRKV	2107	ESEFQAALSRKVAEL	1976	0.0005	0.7400	0.0430		
LGEVPAAES	2108	EVTLGEVPAAESPDP	1977					
VIFSKASSS	2109	FFPVIFSKASSSLQL	1978					
IFSKASSSL	2110	FPVIFSKASSSLQLV	1979					
LGLVGAQAP	2111	GEALGLVGAQAPATE	1980					
YIFATCLGL	2112	GHLYIFATCLGLSYD	1981		0.0025			
LMEVDPIGH	2113	GIELMEVDPIGHLYI	1982					
IIVLAIIAR	2114	GLLIIVLAIIAREGD	1983					
ISYPPLHEW	2115	GPHISYPPLHEWVLR	1984		-0.0018			
LLKYRAREP	2116	HFLLLKYRAREPVTK	1985					
IFATCLGLS	2117	HLYIFATCLGLSYDG	1986					
MEVDPIGHL	2118	IELMEVDPIGHLYIF	1987	0.0130	0.0027	0.0130		
LYIFATCLG	2119	IGHLYIFATCLGLSY	1988					
MLGSVVGNW	2120	KAEMLGSVVGNWQYF	1989					
LLIIVLAII	2121	KAGLLIIVLAIIARE	1990		-0.0011			
LTQHFVQEN	2122	KKLLTQHFVQENYLE	1991					
VPAAESPDP	2123	LGEVPAAESPDPPQS	1992					
VGAQAPATE	2124	LGLVGAQAPATEEQE	1993					
VLAIIAREG	2125	LIIVLAIIAREGDCA	1994					
IVLAIIARE	2126	LLIIVLAIIAREGDC	1995		-0.0018			
YRAREPVTK	2127	LLKYRAREPVTKAEM	1996					
VFGIELMEV	2128	LQLVFGIELMEVDPI	1997	0.0004	0.0970	-0.0004		
VTLGEVPAA	2129	LVEVTLGEVPAAESP	1998					
MPKAGLLII	2130	NQIMPKAGLLIIVLA	1999		-0.0011			
YFFPVIFSK	2131	NWQYFFPVIFSKASS	2000	-0.0003	0.0560	0.2200		
FPDLESEFQ	2132	PSTFPDLESEFQAAL	2001					
FSKASSSLQ	2133	PVIFSKASSSLQLVF	2002	0.0240	0.0890	0.0038		
LSRKVAELV	2134	QAALSRKVAELVHFL	2003					
VQENYLEYR	2135	QHFVQENYLEYRQVP	2004					
FGIELMEVD	2136	QLVFGIELMEVDPIG	2005					
FPVIFSKAS	2137	QYFFPVIFSKASSSL	2006					
VETSYVKVL	2138	RALVETSYVKVLHHM	2007					
VTKAEMLGS	2139	REPVTKAEMLGSVVG	2008					
LVEVTLGEV	2140	SSTLVEVTLGEVPAA	2009					
LVHFLLLKY	2141	VAELVHFLLLKYRAR	2010					
IGHLYIFAT	2142	VDPIGHLYIFATCLG	2011					
IELMEVDPI	2143	VFGIELMEVDPIGHL	2012					
WQYFFPVIF	2144	VGNWQYFFPVIFSKA	2013					
LSVLEVFEG	2145	WEELSVLEVFEGRED	2014					
LWGPRALVE	2146	YEFLWGPRALVETSY	2015					
LHEWVLREG	2147	YPPLHEWVLREGEE-	2016					
VPGSDPACY	2148	YRQVPGSDPACYEFL	2017					
VLHHMVKIS	2149	YVKVLHHMVKISGGP	2018					

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Table XXa A

Mage 2 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSYDGLLGD	2150	CLGLSYDGLLGDNQV	2019	183				0.1400				
IWEELSMLE	2151	EEKIWEELSMLEVFE	2020	220				0.0130				
LESEFQAAI	2152	FPDLESEFQAAISRK	2021	100				0.0033				
MFPDLESEF	2153	GPRMFPDLESEFQAA	2022	96				0.0890				
IEGDCAPEE	2154	IIAIEGDCAPEEKIW	2023	210				0.0660				
IAIEGDCAP	2155	LAIIAIEGDCAPEEK	2024	208				0.0190				
LVQENYLEY	2156	MQDLVQENYLEYRQV	2025	249				0.2000				
FGIEVVEVV	2157	QLVFGIEVVEVVPIS	2026	161				0.0072				
LMQDLVQEN	2158	RKLLMQDLVQENYLE	2027	245				0.1500				
LLGDNQVMP	2159	YDGLLGDNQVMPKTG	2028	188				0.0270				

Table XXa A

Mage 2 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSYDGLLGD	2150	CLGLSYDGLLGDNQV	2019					
IWEELSMLE	2151	EEKIWEELSMLEVFE	2020					
LESEFQAAI	2152	FPDLESEFQAAISRK	2021					
MFPDLESEF	2153	GPRMFPDLESEFQAA	2022					
IEGDCAPEE	2154	IIAIEGDCAPEEKIW	2023					
IAIEGDCAP	2155	LAIIAIEGDCAPEEK	2024					
LVQENYLEY	2156	MQDLVQENYLEYRQV	2025					
FGIEVVEVV	2157	QLVFGIEVVEVVPIS	2026					
LMQDLVQEN	2158	RKLLMQDLVQENYLE	2027					
LLGDNQVMP	2159	YDGLLGDNQVMPKTG	2028					

Table XXa B

Mage 3 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSYDGLLGD	2160	CLGLSYDGLLGDNQI	2029	183				-0.0025				
IWEELSVLE	2161	EEKIWEELSVLEVFE	2030	220				0.0058				
LESEFQAAL	2162	FPDLESEFQAALSRK	2031	100				0.0026				
MEVDPIGHL	2163	IELMEVDPIGHLYIF	2032	166	0.0003	0.0057	-0.0010	1.8000	-0.0055		-0.0008	
IAREGDCAP	2164	LAIIAREGDCAPEEK	2033	208				-0.0025				
FGIELMEVD	2165	QLVFGIELMEVDPIG	2034	161				0.0150				
FVQENYLEY	2166	TQHFVQENYLEYRQV	2035	249				0.2800				
LLGDNQIMP	2167	YDGLLGDNQIMPKAG	2036	188				0.0080				

Table XXa B

Mage 3 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSYDGLLGD	2160	CLGLSYDGLLGDNQI	2029					
IWEELSVLE	2161	EEKIWEELSVLEVFE	2030					
LESEFQAAL	2162	FPDLESEFQAALSRK	2031					
MEVDPIGHL	2163	IELMEVDPIGHLYIF	2032	0.0130	0.0027	0.0130		
IAREGDCAP	2164	LAIIAREGDCAPEEK	2033					
FGIELMEVD	2165	QLVFGIELMEVDPIG	2034					
FVQENYLEY	2166	TQHFVQENYLEYRQV	2035					
LLGDNQIMP	2167	YDGLLGDNQIMPKAG	2036					

Table XXb A

Mage 2 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
AAISRKMVE	2168	EFQAAISRKMVELVH	2037	106				0.0039				
MPLEQRSQH	2169	MPLEQRSQHCKP	2038	1								
IGGEPHISY	2170	TLKIGGEPHISYPPL	2039	292				-0.0025				
LHHTLKIGG	2171	VKVLHHTLKIGGEPH	2040	286				-0.0025				

Table XXb A

Mage 2 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
AAISRKMVE	2168	EFQAAISRKMVELVH	2037					
MPLEQRSQH	2169	MPLEQRSQHCKP	2038					
IGGEPHISY	2170	TLKIGGEPHISYPPL	2039					
LHHTLKIGG	2171	VKVLHHTLKIGGEPH	2040					

Table XXb B

Mage 3 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2β1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
ILGDPKKLL	2172	EDSILGDPKKLLTQH	2041	237	0.0003	-0.0006	-0.0010	0.6700	-0.0055		-0.0008	
AALSRKVAE	2173	EFQAALSRKVAELVH	2042	106				0.0027				
MPLEQRSQH	2174	MPLEQRSQHCKP	2043	1								

Table XXb B

Mage 3 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
ILGDPKKLL	2172	EDSILGDPKKLLTQH	2041	0.0130	-0.0014	0.0029		
AALSRKVAE	2173	EFQAALSRKVAELVH	2042					
MPLEQRSQH	2174	MPLEQRSQHCKP	2043					

Table XXII. A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
MAGE3.112	9	KVAELVHFL	2214	69	29	14	168	17	5
MAGE3.112L2	9	KLAELVHFL	2215	20	6.0	5.9	12	400	5
MAGE3.112M2	9	KMAELVHFL	2216	24	6.7	7.7	26	286	5
MAGE3.112L2V9	9	KLAELVHFV	2217	14	13	22	15	73	5
MAGE3.112M2V9	9	KMAELVHFV	2218	26	17	46	39	170	5
MAGE3.220	9	KIWEELSVL	2219	333	391	2381	308	--	3
MAGE3.220L2V9	9	KLWEELSVV	2220	11	165	20	15	--	4

-- indicates binding affinity =10,000nM.

Table XXIIA A01 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0101 nM
52.0026	8	ATCLGLSY	2221	MAGE3.179	227.3
52.013	11	VVEVVPISHLY	2222	MAGE2.166	125
52.0132	11	TMNYPLWSQSY	2223	MAGE3.74	301.2
52.0133	11	LMEVDPIGHLY	2224	MAGE3.166	3.3
57.0003	8	VTDLGLSY	2225	MAGE2.179.D3	2.7
57.0029	9	STFSTTINY	2226	MAGE2.69.T2	490.2
57.003	9	MTDLVQENY	2227	MAGE2.247.T2	0.8
57.0031	9	STLPTTMNY	2228	MAGE3.69.T2	58.1
57.0032	9	GTVVGNWQY	2229	MAGE3.137.T2	36.2
57.0033	9	ETDPIGHLY	2230	MAGE3.168.T2	0.7
57.0034	9	ITGGPHISY	2231	MAGE3.293.T2	36.2
57.0119	10	ATSFSTTINY	2232	MAGE2.68.T2	454.5
57.012	10	ASDFSTTINY	2233	MAGE2.68.D3	25
57.0121	10	LTQDLVQENY	2234	MAGE2.246.T2	58.1
57.0122	10	ATSLPTTMNY	2235	MAGE3.68.T2	208.3
57.0123	10	ASDLPTTMNY	2236	MAGE3.68.D3	2.6
57.0124	10	LTDHFVQENY	2237	MAGE3.246.D3	2.3

Table XXIIB A03 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.63	9	SVFSTTINK	2238	MAGE2.69.V2K9	20	8.2	3333.3	9666.7	5.7	3
1371.64	9	SVFSTTINR	2239	MAGE2.69.V2R9	57.9	6.3	62.1	87.9	6.7	5
1371.65	9	TVINYTLWR	2240	MAGE2.73.V2	261.9	76.9	720	432.8	14.5	4
1371.66	9	TVINYTLWK	2241	MAGE2.73.V2K9	305.6	96.8	9000	-58000	61.5	3
1371.68	9	LVHFLLLKR	2242	MAGE2/3.116.R9	440	375	236.8	93.5	26.7	5
1371.69	9	YVFPVIFSK	2243	MAGE3.138.V2	24.4	3	2769.2	783.8	1.7	3
1371.7	9	YVFPVIFSR	2244	MAGE3.138.V2R9	35.5	2.6	6	13.2	0.5	5
1371.71	8	SVFAHPRR	2245	MAGE2.237.R8	687.5	1538.5	620.7	580	156.9	1
1371.72	9	AVIETSYVK	2246	MAGE2.277.V2	392.9	62.5	12857.1	-290000	30.8	3
1371.73	9	AVIETSYVR	2247	MAGE2.277.V2R9	36666.7	171.4	128.6	1160	15.4	3
1371.74	9	IVYPPLHER	2248	MAGE2.299.V2	117	375	94.7	32.2	13.8	5
1371.75	9	IVYPPLHEK	2249	MAGE2.299.V2K9	42.3	103.4	857.1	2989.7	42.1	3

Table XXIIC A24 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*2401 nM
52.0072	8	LWGPRALI	2250	MAGE2.272	100
52.0073	8	QYFFPVIF	2251	MAGE3.144	100
52.0078	8	SYPPLHEW	2252	MAGE3.300	285.7
52.0102	10	SYPPLHEWVL	2253	MAGE3.300	20.3
52.0166	11	SFSTTINYTLW	2254	MAGE2.70	428.6
52.0167	11	IFSKASEYLQL	2255	MAGE2.150	126.3
52.017	11	IFSKASSSLQL	2256	MAGE3.150	131.9
52.0172	11	IWEELSVLEVF	2257	MAGE3.221	461.5
57.006	9	MYPDLESEF	2258	MAGE2.97.Y2	52.2
57.0061	9	KYVELVHFF	2259	MAGE2.112.Y2F9	7.1
57.0062	9	IYSKASEYF	2260	MAGE2.150.Y2F9	14.6
57.0063	9	EYLQLVFGF	2261	MAGE2.156.F9	4
57.0064	9	VYPKTGLLF	2262	MAGE2.195.Y2F9	5.5
57.0065	9	TYPDLESEF	2263	MAGE3.97.Y2	218.2
57.0066	9	NYQYFFPVF	2264	MAGE3.142.Y2F9	3.4
57.0067	9	IYSKASSSF	2265	MAGE3.150.Y2F9	375
57.0068	9	IYPKAGLLF	2266	MAGE3.195.Y2F9	9.2
57.0084	10	SYSTTINYTF	2267	MAGE2.70.Y2F10	14.8
57.0085	10	LYILVTCLGF	2268	MAGE2.175.F10	17.6
57.0086	10	VYPKTGLLIF	2269	MAGE2.195.Y2F10	2.9
57.0087	10	EYLWGPRALF	2270	MAGE2.270.Y2F10	10
57.0088	10	SYVKVLHHTF	2271	MAGE2.282.F10	34.3
57.009	10	NYQYFFPVIF	2272	MAGE3.142.Y2	22.6
57.0092	10	LYIFATCLGF	2273	MAGE3.175.F10	10
57.0093	10	IYPKAGLLIF	2274	MAGE3.195.Y2F10	1.2
57.0095	10	SYPPLHEWVF	2275	MAGE3.300.F10	5.5

Table XXIII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type [1]	CTL Tumor
MAGE2.112	9	KMVELVHFL	2276	9.8	25	17	123	2353	4	1/1	0/1
MAGE2.112	10	KMVELVHFLL	2277	23	39	127	9.0	2667	4	1/1	0/1
MAGE2.112	11	KMVELVHFLLL	2278	5.0	45	63	109	7692	4	1/1	0/1
MAGE2.153	9	KASEYLQLV	2279	152	116	17	185	4878	4	2/4	0/2
MAGE2.157	10	YLQLVFGIEV	2280	50	165	345	370	9302	4	3/3	1/3
MAGE2.160	10	LVFGIEVVEV	2281	357	20	43	28	8.0	5	4/4	0/3
MAGE3.112	9	KVAELVHFL	2282	68	29	14	168	17	5	3/4	3/4
MAGE3.112	10	KVAELVHFLL	2283	54	36	217	206	11	5	0/1	0/1
MAGE3.159	11	QLVFGIELMEV	2284	7.9	74	217	185	267	5	3/3	1/3 [2]
MAGE3.160	10	LVFGIELMEV	2285	29	20	7.7	28	14	5	4/4	1/4 [2]
MAGE3.195	11	IMPKAGLLIIV	2286	20	226	14	176	-- [3]	4	3/4	0/3
MAGE3.220	9	KIWEELSVL	2287	357	391	2381	308	--	3	3/4	0/3
MAGE3.271	9	FLWGPRALV	2288	31	43	14	336	40	5	4/4	2/4

1) Indicates the number of donors positive over the total number of donors tested.
2) A positive result was seen after the second restim.
3) -- indicates binding affinity =10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		
				Source	Sequence	SEQ ID NO:
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	2289
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV	2290
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	2291
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	2292
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	2293
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	2294
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	2295
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	2296
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	2297
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	2298
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	2299
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVRR	2300
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	2301
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVYLL	2302
	B8	B*0801	Steinlin	HIVgp 586-593 Y1->F, Q5->Y	FLKDYQLL	2303
	B27	B*2705	LG2	R 60s	FRYNGLIHR	2304
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF	2305
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	2306
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	2307
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	2308
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	2309
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	2310
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	2311
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL	2312
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	2313
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	2314
Mouse	D^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	2315
	K^b		EL4	VSV NP 52-59	RGYVFQGL	2316
	D^d		P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	2317
	K^d		P815	non-natural (KdCON1)	KFNPMKTYI	2318
	L^d		P815	HBVs 28-39	IPQSLDSYWTSL	2319

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		SEQ ID NO:
				Source	Sequence	
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVKQNTLKLAT	2320
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY	2321
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAAAFA	2322
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR	2323
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	2324
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	2325
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	2326
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	2327
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE	2328
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE	2329
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE	2330
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE	2331
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE	2332
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS	2333
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE	2334
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE	2335
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVKQNTLKLAT	2336
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL	2337
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT	2338
	DQ3.1	QA1*0301/DQB1*03(	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2339
Mouse	IA^b		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2340
	IA^d		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2341
	IA^k		CH-12	HEL 46-61	YNTDGSTDYGILQINSR	2342
	IA^s		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2343
	IA^u		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2344
	IE^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK	2345
	IE^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK	2346

Table XXVI. Crossbinding data A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
MAGE2.112	9	KMVELVHFL	2347	38	15	9.1	49	364	5
MAGE2.112	10	KMVELVHFLL	2348	23	39	127	9.0	2667	4
MAGE2.112	11	KMVELVHFLLL	2349	5.0	45	63	109	7692	4
MAGE2.153	9	KASEYLQLV	2350	152	116	17	185	4878	4
MAGE2.157	10	YLQLVFGIEV	2351	50	165	345	370	9302	4
MAGE2.160	10	LVFGIEVVEV	2352	357	21	44	29	8.0	5
MAGE2.220	9	KIWEELSML	2353	167	642	175	29	--	3
MAGE2.271	9	FLWGPRALI	2354	238	96	137	1542	95	4
MAGE2.277	10	ALIETSYVKV	2355	500	729	125	1947	3077	2
MAGE2/3.44	10	TLVEVTLGEV	2356	67	39	4.3	218	33	5
MAGE3.112	9	KVAELVHFL	2357	68	29	14	168	17	5
MAGE3.112	10	KVAELVHFLL	2358	54	36	217	206	11	5
MAGE3.159	11	QLVFGIELMEV	2359	7.9	74	217	185	267	5
MAGE3.160	10	LVFGIELMEV	2360	29	20	7.7	29	14	5
MAGE3.174	11	HLYIFATCLGL	2361	56	741	769	--	4494	1
MAGE3.176	9	YIFATCLGL	2362	185	45	37	1028	222	4
MAGE3.195	11	IMPKAGLLIIV	2363	20	226	15	176	--	4
MAGE3.220	9	KIWEELSVL	2364	333	391	2381	308	--	3
MAGE3.271	9	FLWGPRALV	2365	31	43	14	336	40	5

-- indicates binding affinity =10,000nM.

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type [1]	CTL Tumor
MAGE2.112	9	KMVELVHFL	2366	9.8	25	17	123	2353	4	1/1	0/1
MAGE2.112	10	KMVELVHFLL	2367	23	39	127	9.0	2667	4	1/1	0/1
MAGE2.112	11	KMVELVHFLLL	2368	5.0	45	63	109	7692	4	1/1	0/1
MAGE2.153	9	KASEYLQLV	2369	152	116	17	185	4878	4	2/4	0/2
MAGE2.157	10	YLQLVFGIEV	2370	50	165	345	370	9302	4	3/3	1/3
MAGE2.160	10	LVFGIEVVEV	2371	357	20	43	28	8.0	5	4/4	0/3
MAGE3.112	9	KVAELVHFL	2372	68	29	14	168	17	5	3/4	3/4
MAGE3.112	10	KVAELVHFLL	2373	54	36	217	206	11	5	0/1	0/1
MAGE3.159	11	QLVFGIELMEV	2374	7.9	74	217	185	267	5	3/3	1/3[2]
MAGE3.160	10	LVFGIELMEV	2375	29	20	7.7	28	14	5	4/4	1/4[2]
MAGE3.195	11	IMPKAGLLIIV	2376	20	226	14	176	--[3]	4	3/4	0/3
MAGE3.220	9	KIWEELSVL	2377	357	391	2381	308	--	3	3/4	0/3
MAGE3.271	9	FLWGPRALV	2378	31	43	14	336	40	5	4/4	2/4

1) Indicates the number of donors positive over the total number of donors tested.
2) A positive result was seen after the second restim.
3) -- indicates binding affinity =10,000nM.

Table XXVIII. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross-binding
39.0282	2	LGEVPAADSPSPPHS	2379	MAGE2.50	--	--	--	0
39.0283	3	ESEFQAAISRKMVEL	2380	MAGE2.102	4.2	281	49	3
39.0284	2	GIEVVEVVPISHLYI	2381	MAGE2.163	595	6429	278	2
39.0285	2	DGLLGDNQVMPKTGL	2382	MAGE2.187	--	--	--	0
39.0286	2	NQVMPKTGLLIIVLA	2383	MAGE2.193	2632	--	--	0
39.0287	2	KTGLLIIVLAIIAIE	2384	MAGE2.198	417	1216	862	2
39.0288	2	TGLLIIVLAIIAIEG	2385	MAGE2.199	6250	--	--	0
39.0291	2	GLLIIVLAIIAIEGD	2386	MAGE2.200	500	--	--	1
39.0292	3	LLIIVLAIIAIEGDC	2387	MAGE2.201	581	3750	1923	1
39.0293	2	LIIVLAIIAIEGDCA	2388	MAGE2.202	417	8824	2083	1
39.0294	2	EPHISYPPLHERALR	2389	MAGE2.296	--	--	--	0
39.0295	3	ALGLVGAQAPATEEQ	2390	MAGE2/3.22	152	--	--	1
39.0296	2	ESEFQAALSRKVAEL	2391	MAGE3.102	2.6	763	34	3
39.0297	2	NWQYFFPVIFSKASS	2392	MAGE3.142	46	409	446	3
39.0298	3	PVIFSKASSSLQLVF	2393	MAGE3.148	98	1875	281	2
39.0299	3	LQLVFGIELMEVDPI	2394	MAGE3.158	200	--	258	2
39.0300	3	GHLYIFATCLGLSYD	2395	MAGE3.173	455	4091	--	1
39.0301	2	DGLLGDNQIMPKAGL	2396	MAGE3.187	--	--	--	0
39.0302	2	NQIMPKAGLLIIVLA	2397	MAGE3.193	114	--	--	1
39.0303	2	KAGLLIIVLAIIARE	2398	MAGE3.198	1163	--	--	0
39.0304	2	AGLLIIVLAIIAREG	2399	MAGE3.199	1111	--	>9615	0
39.0305	3	LLIIVLAIIAREGDC	2400	MAGE3.201	1923	--	--	0
39.0306	2	GPHISYPPLHEWVLR	2401	MAGE3.296	2273	--	--	0

-- indicates binding affinity =10,000nM.

Table XXIX. DR supertype crossbinding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 β1 nM	DR2w2 β2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR 147 Cross-binding	Broad Binding (5/8)
39.0283	ESEFQAAISRKMVEL	2402	MAGE2.102	4.2	281	49	147	20	522	741	1581	3	7
39.0284	GIEVVEVVPISHLYI	2403	MAGE2.163	595	6429	278	1978	--	49	--	5506	2	3
39.0287	KTGLLIIVLAIIAIE	2404	MAGE2.198	417	1216	862	2460	--	2333	--	--	2	2
39.0296	ESEFQAALSRKVAEL	2405	MAGE3.102	2.6	763	34	29	18	7000	645	1140	3	6
39.0297	NWQYFFPVIFSKASS	2406	MAGE3.142	46	409	446	3033	667	--	308	223	3	6
39.0298	PVIFSKASSSLQLVF	2407	MAGE3.148	98	1875	281	535	--	146	--	--	2	4
39.0299	LQLVFGIELMEVDPI	2408	MAGE3.158	200	--	258	4550	--	8750	--	--	2	2

-- indicates binding affinity =10,000nM.

Table XXX. DR3 binding

Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0384	GPRMFPDLESEFQAA	2409	MAGE2.94	3371
39.0387	FPDLESEFQAAISRK	2410	MAGE2.98	--
39.0388	EFQAAISRKMVELVH	2411	MAGE2.104	--
39.0389	QLVFGIEVVEVVPIS	2412	MAGE2.159	--
39.0390	CLGLSYDGLLGDNQV	2413	MAGE2.181	2143
39.0391	YDGLLGDNQVMPKTG	2414	MAGE2.186	--
39.0392	LAIIAIEGDCAPEEK	2415	MAGE2.206	--
39.0393	IIAIEGDCAPEEKIW	2416	MAGE2.208	4546
39.0394	EEKIWEELSMLEVFE	2417	MAGE2.218	--
39.0395	RKLLMQDLVQENYLE	2418	MAGE2.243	2000
39.0396	MQDLVQENYLEYRQV	2419	MAGE2.247	1500
39.0397	VKVLHHTLKIGGEPH	2420	MAGE2.284	--
39.0398	TLKIGGEPHISYPPL	2421	MAGE2.290	--
39.0399	FPDLESEFQAALSRK	2422	MAGE3.98	--
39.0400	EFQAALSRKVAELVH	2423	MAGE3.104	--
39.0401	QLVFGIELMEVDPIG	2424	MAGE3.159	--
39.0402	IELMEVDPIGHLYIF	2425	MAGE3.164	167
39.0403	CLGLSYDGLLGDNQI	2426	MAGE3.181	--
39.0404	YDGLLGDNQIMPKAG	2427	MAGE3.186	--
39.0405	LAIIAREGDCAPEEK	2428	MAGE3.206	--
39.0406	EEKIWEELSVLEVFE	2429	MAGE3.218	--
39.0407	EDSILGDPKKLLTQH	2430	MAGE3.235	448
39.0408	TQHFVQENYLEYRQV	2431	MAGE3.247	1071

-- indicates binding affinity =10,000nM.

Table XXXI. HTL Candidates

Peptide	Sequence	SEQ ID NO:	Motif	Source	DR1 nM	DR4w4 nM	DR7 nM	DR3 nM	DR2w2 β1 nM	DR2w2 β2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR 147 Cross-binding	Broad Binding (5/8)	DR3 Binder
39.0283	ESEFQAAISRKMVEL	2432	DR sup	MAGE2.102	4.2	281	49	--	147	20	522	741	1581	3	7	0
39.0296	ESEFQAALSRKVAEL	2433	DR sup	MAGE3.102	3	763	34	--	29	18	7000	645	1140	3	6	0
39.0297	NWQYFFPVIFSKASS	2434	DR sup	MAGE3.142	46	409	446	--	3033	667	--	308	223	3	6	0
39.0402	IELMEVDPIGHLYIF	2435	DR3	MAGE3.164	--	>8182	9259	167	1597	--	269	--	3769	0	1	1
39.0407	EDSILGDPKKLLTQH	2436	DR3	MAGE3.235	--	>8182	--	448	--	--	269	--	--	0	1	1

-- indicates binding affinity =10,000nM.